

Table 1

PhageTech

Database

Genome Sequence

>sid|300001 Phage 77 Complete genome 41708 bases 16-10-1998

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ORF record

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40321 tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaaat aaacgatt
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40461 aaagaattat tattaattta aacaagagga gatttaaatt atgtggatta ctatgactat tgtatttg
40531 atattgctat tagtttgtat cagtattaat agtgatcgtg caagagagat acaagcactt agatatat
40601 atgattatct acttgatgaa gtagttaaaa ctaaaaggta caacgggtta gaagaatata ggattgaa
40671 gaagcgaatg aataacgata ttaaaaagta atttatatta tcggagggtat tgcattgaat gataaaga
40741 gagaaacacg atatcaaaaa gcttgaagaa tacattcagc acatcgataa ctatcgaaga gagttgaa
40811 tgcgagaata tgaattactt gaaagtcag aaccagataa tgcgggagct ggcaaaagta atttgccg
40881 taaccgcgatt gaacgatgtg caataaagaa gtttagtgat aacagggtaca atacattaag aatatag
40951 aacggtgtag atagattgat aggtgaaagt gatgaggata cgcttgagtt attaaggttt agatattg
41021 attgtcctat tggttgttat gaatgggaag atatagcaca ttacttttgt acaagtaaga caagtata
41091 acgtagaagg aatgcactga tcgataagtt agcaaagtat attggttatg tgtagcggac ttttacc
41161 tgtaagtcog cattaaaaca gtttattatg ttagtatcag attaatattt aaagttatta atgtcta
41231 cgacgcgatga acaagaggcg catcactatg tgatgtgtct ttttatttat gaggtatgaa catgttca
41301 ctaattgtaa atacattact acacatcaag tatagatgag tcttgatact acttaagtta tataaggt
41371 aacattatga tgactaaaga cgaacgtata cgattctata agtctaaaga atggcaaata acaagaaa
41441 gagtgctaga aagagataat tatgaatgtc aacaatgtaa gagagacggc aagttaacga catatgac
41511 aagcaagcgt aagtcgttgg atgtagatca tatattatcg ctagaacatc atccggagtt tgctcatg
41581 ttaaacaatt tagaaacact gtgtattaaa tgtcacaaca aaaaagaaaa gagatttata aaaaaga
41651 ataaatggaa agacgaaaaa tggtaaatac ccccggttca aaaaaatcaa aagcgatc

```

Table 2

1st position (5' end) ↓	2nd position				3rd position (3' end) ↓
	U	C	A	G	
U	Phe Phe Leu Leu	Ser Ser Ser Ser	Tyr Tyr STOP STOP	Cys Cys STOP Trp	U C A G
C	Leu Leu Leu Leu	Pro Pro Pro Pro	His His Gln Gln	Arg Arg Arg Arg	U C A G
A	Ile Ile Ile Met	Thr Thr Thr Thr	Asn Asn Lys Lys	Ser Ser Arg Arg	U C A G
G	Val Val Val Val	Ala Ala Ala Ala	Asp Asp Glu Glu	Gly Gly Gly Gly	U C A G

Figure 3-16 The genetic code. Sets of three nucleotides (*codons*) in an mRNA molecule are translated into amino acids in the course of protein synthesis according to the rules shown. The codons GUG and GAG, for example, are translated into valine and glutamic acid, respectively. Note that those codons with U or C as the second nucleotide tend to specify the more hydrophobic amino acids

77ORF017 sequence

23982 atgacgcataatatagaaaaacgcattaataaattaaaaaacttct
1 M T H N I E K R I N K L K T S
23937 ggaaatccaaaattttaaaaagtttagattcagatattcactattta
16 G N P K F K K L D S D I H Y L
23892 ctcaagagatttgaaggtgaaaaaaaccataaagggtttttatcca
31 L K R F E G E K N H K G F Y P
23847 aagtttaaacaaaggagaaatagtttttgtagatttcggtataaac
46 K F K Q G E I V F V D F G I N
23802 gttaataaagaatttttctaattcacacttttgcaatagtgatgaat
61 V N K E F S N S H F A I V M N
23757 aaaaatgatttctaatacggaggatatagtaaagtgttattccctta
76 K N D S N T E D I V N V I P L
23712 tcctctaagaaaaacaaaaagtattttaagatgaatttttgattg
91 S S K E N K K Y L K M N F D L
23667 aaatgggagttattttaaagattgtttttaaatttaattagcgcg
106 K W E Y Y L R L F L N L I S A
23622 caaaataattcagctatatattaaagaagttttcgataaaaaaatac
121 Q N N S A I L K E V F D K K Y
23577 caaaaaaacacacagaattcatcactaaagattattttattgaa
136 Q K N N T E F I T K D Y F I E
23532 tttatatctgatagtttagaaattgaaaataaattaaataaaatt
151 F I S D S L E I E N K L N K I
23487 gacagaaacattaataacatagtatcagcaattgataaggtaaaa
166 D R N I N N I V S A I D K V K
23442 aaattaaaaggtaatagttacgcttgcataaattctttccagccg
181 K L K G N S Y A C I N S F Q P
23397 attagtaagtttcgcataagaaaagttttacccccaaaaaattaaa
196 I S K F R I R K V L P Q K I K
23352 aatccagataatagattcttcggatattatgttactgataaataga
211 N P V I D S S D I M L L I N R
23307 attaataataatatattgcagatccctgatataagatga 23269
226 I N N N I L O I P D I R *

Physico-chemical parameters of ORF 77ORF017

```

1      MTHNIEKRIN KLKTSGNPKF KKLDSDIHYL LKRFEGEKNH KGFYPKFKQG EIVFVDFGIN
61     VNKEFSNSHF AIVMNKNSN TEDI NVIPL SSKENKKYLK MNFDLKWEYY LRLFLNLISA
121    QNNSAILKEV FDKKYQKNNT EFITKDYFIE FIDSLEIEN KLNKIDRNIN NIVSAIDKVK
181    KLKGNSYACI NSFQISKFR IRKVL PQIK NPVIDSSDIM LLINRINNNI LQIPDIR
  
```

Number of amino acids: 237
 Average molecular weight (Daltons): 27887.38
 Mean amino acid weight (Daltons): 117.67
 Monoisotopic molecular weight (Daltons): 27869.83
 Mean amino acid monoisotopic weight (Daltons): 117.59

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	5	2.11%	7.58%	Cys	C	1	0.42%	1.66%
Asp	D	14	5.91%	5.28%	Glu	E	13	5.49%	6.37%
Phe	F	16	6.75%	4.09%	Gly	G	6	2.53%	6.84%
His	H	4	1.69%	2.24%	Ile	I	29	12.24%	5.81%
Lys	K	33	13.92%	5.95%	Leu	L	19	8.02%	9.42%
Met	M	4	1.69%	2.37%	Asn	N	30	12.66%	4.45%
Pro	P	7	2.95%	4.9%	Gln	Q	6	2.53%	3.97%
Arg	R	8	3.38%	5.16%	Ser	S	17	7.17%	7.12%
Thr	T	5	2.11%	5.67%	Val	V	11	4.64%	6.58%
Trp	W	1	0.42%	1.23%	Tyr	Y	8	3.38%	3.18%

Number of acidic (negative) amino acids (ED): 27 11.39%
 Number of basic (positive) amino acids (KR): 41 17.30%
 Total charge (KRED): 68 28.69%
 Net charge (KR - ED): 14 5.91%
 Theoretical pI: 10.01
 Total linear charge density: 0.30
 Average hydrophobicity: -5.37
 Ratio of hydrophilicity to hydrophobicity: 1.41
 Percentage of hydrophilic amino acid: 57.81%
 Percentage of hydrophobic amino acid: 42.19%
 Ratio of %hydrophilic to %hydrophobic: 1.37

77ORF019 sequence

```

39851 atgaacgagcaaataataggaagcatatatacttttagcaggaggt
1   M N E Q I I G S I Y T L A G G
39896 gttgtgctttattcagttaaagagattttttaggtattttacagat
16  V V L Y S V K E I F R Y F T D
39941 tctaacttacaacgtaaaaaaatcaatttagaacaatatatccg
31  S N L Q R K K I N L E Q I Y P
39986 atatatttagattgttttaaaaaggctaaaaagatgattggagct
46  I Y L D C F K K A K K M I G A
40031 tatattattccaacagacagcatgaatttttagatttttttgat
61  Y I I P T E Q H E F L D F F D
40076 attgaagtctttaataatttagataagcaaaagtaaaaaagcgtat
76  I E V F N N L D K Q S K K A Y
40121 gaaaatgttattggatttagacaaatgattaattttatcaaataga
91  E N V I G F R Q M I N L S N R
40166 gttaaggcaatggaagattttaagatgagtttcaacaatgaattt
106 V K A M E D F K M S F N N E F
40211 agtacaaatcagatttttttaataccttcttttgttatggaaaca
121 S T N Q I F F N P S F V M E T
40256 attgctattataaatgaatatcaaaaagatatatcttatttataaa
136 I A I I N E Y Q K D I S Y L K
40301 aatataattaataaaaatgaatgaaaatagagcttataatcatatt
151 N I I N K M N E N R A Y N H I
40346 gatagttttatcacttcagagtaccgacgaaaaataaacgattat
166 D S F I T S E Y R R K I N D Y
40391 aatctttatcttgataaatttgaagaacagtttagtcaaaagttt
181 N L Y L D K F E E Q F S Q K F
40436 aaaataaacagaacttcgataaaaagaaagaattattattaattta
196 K I N R T S I K E R I I I N L
40481 aacaaggaggagattttaaata 40501
211 N K R R F K *

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66269-192949

Physico-chemical parameters of ORF 77ORF019

1 MNEQIIGSIY TLAGGVVLYS VKEIFRYFTD SNLQQRKINL EQIYPIYLDK FKKAKKMIGA
61 YIIPTEQHEF LDFFDIEVFN NLDKQSKKAY ENVIGFRQMI NLSNRVKAME DFKMSFNNEF
121 STNQIFFNPS FVMETIAIIN EYQKDISYLK NIINKMNENR AYNHIDSFIT SEYRRKINDY
181 NLYLDKFEEQ FSQKFKINRT SIKERIIINL NKRRFK

Number of amino acids: 216
Average molecular weight (Daltons): 26026.06
Mean amino acid weight (Daltons): 120.49
Monoisotopic molecular weight (Daltons): 26009.34
Mean amino acid monoisotopic weight (Daltons): 120.41

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	7	3.24%	7.58%	Cys	C	1	0.46%	1.66%
Asp	D	10	4.63%	5.28%	Glu	E	16	7.41%	6.37%
Phe	F	19	8.80%	4.09%	Gly	G	5	2.31%	6.84%
His	H	2	0.93%	2.24%	Ile	I	28	12.96%	5.81%
Lys	K	22	10.19%	5.95%	Leu	L	12	5.56%	9.42%
Met	M	7	3.24%	2.37%	Asn	N	23	10.65%	4.45%
Pro	P	3	1.39%	4.9%	Gln	Q	10	4.63%	3.97%
Arg	R	11	5.09%	5.16%	Ser	S	13	6.02%	7.12%
Thr	T	7	3.24%	5.67%	Val	V	7	3.24%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	13	6.02%	3.18%

Number of acidic (negative) amino acids (ED): 26 12.04%
Number of basic (positive) amino acids (KR): 33 15.28%
Total charge (KRED): 59 27.31%
Net charge (KR - ED): 7 3.24%
Theoretical pI: 9.52
Total linear charge density: 0.28
Average hydrophobicity: -4.84
Ratio of hydrophilicity to hydrophobicity: 1.37
Percentage of hydrophilic amino acid: 54.17%
Percentage of hydrophobic amino acid: 45.83%
Ratio of %hydrophilic to %hydrophobic: 1.18

[illegible][illegible]

Physico-chemical parameters of ORF 77ORF043

1 MYYEIGEIIIR KNIHVNGFDF KLFILKGHMG ISIQVKDMNN VPIKHAYVVD ENLDLMASDL
61 FNQAIDEWIE ENTDEQDRLI NLVMKW

Number of amino acids: 86
Average molecular weight (Daltons): 10186.68
Mean amino acid weight (Daltons): 118.45
Monoisotopic molecular weight (Daltons): 10180.02
Mean amino acid monoisotopic weight (Daltons): 118.37

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	3	3.49%	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	10.47%	5.28%	Glu	E	7	8.14%	6.37%
Phe	F	4	4.65%	4.09%	Gly	G	4	4.65%	6.84%
His	H	3	3.49%	2.24%	Ile	I	11	12.79%	5.81%
Lys	K	6	6.98%	5.95%	Leu	L	6	6.98%	9.42%
Met	M	5	5.81%	2.37%	Asn	N	8	9.30%	4.45%
Pro	P	1	1.16%	4.9%	Gln	Q	3	3.49%	3.97%
Arg	R	2	2.33%	5.16%	Ser	S	2	2.33%	7.12%
Thr	T	1	1.16%	5.67%	Val	V	6	6.98%	6.58%
Trp	W	2	2.33%	1.23%	Tyr	Y	3	3.49%	3.18%

Number of acidic (negative) amino acids (ED): 16 18.60%
Number of basic (positive) amino acids (KR): 8 9.30%
Total charge (KRED): 24 27.91%
Net charge (KR - ED): -8 -9.30%
Theoretical pI: 4.38
Total linear charge density: 0.30
Average hydrophobicity: -2.80
Ratio of hydrophilicity to hydrophobicity: 1.19
Percentage of hydrophilic amino acid: 48.84%
Percentage of hydrophobic amino acid: 51.16%
Ratio of %hydrophilic to %hydrophobic: 0.95

[illegible]

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29051 atgagcaacattttataaaaagctacctagtagcagtattatgcttc
1      M  S  N  I  Y  K  S  Y  L  V  A  V  L  C  F
29096 acagtcttagcgattgtactttatgccgtttctatacttcactaca
16     T  V  L  A  I  V  L  M  P  F  L  Y  F  T  T
29141 gcatggtcaattgcgggattcgcaagtatcgcaacattcatgtac
31     A  W  S  I  A  G  F  A  S  I  A  T  F  M  Y
29186 tacaaagaatgctttttcaaagaataa 29212
46     Y  K  E  C  F  F  K  E  *

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Physico-chemical parameters of ORF 77ORF102

1 MSNIYKSYLV AVLCTVLAI VLMPFLYFTT AWSIAGFASI ATFMYYKECF FKE

Number of amino acids: 53
Average molecular weight (Daltons): 6155.42
Mean amino acid weight (Daltons): 116.14
Monoisotopic molecular weight (Daltons): 6151.07
Mean amino acid monoisotopic weight (Daltons): 116.06

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	6	11.32%	7.58%	Cys	C	2	3.77%	1.66%
Asp	D	0	0.00%	5.28%	Glu	E	2	3.77%	6.37%
Phe	F	7	13.21%	4.09%	Gly	G	1	1.89%	6.84%
His	H	0	0.00%	2.24%	Ile	I	4	7.55%	5.81%
Lys	K	3	5.66%	5.95%	Leu	L	5	9.43%	9.42%
Met	M	3	5.66%	2.37%	Asn	N	1	1.89%	4.45%
Pro	P	1	1.89%	4.9%	Gln	Q	0	0.00%	3.97%
Arg	R	0	0.00%	5.16%	Ser	S	4	7.55%	7.12%
Thr	T	4	7.55%	5.67%	Val	V	4	7.55%	6.58%
Trp	W	1	1.89%	1.23%	Tyr	Y	5	9.43%	3.18%

Number of acidic (negative) amino acids (ED): 2 3.77%
Number of basic (positive) amino acids (KR): 3 5.66%
Total charge (KRED): 5 9.43%
Net charge (KR - ED): 1 1.89%
Theoretical pI: 8.18
Total linear charge density: 0.13
Average hydrophobicity: 10.81
Ratio of hydrophilicity to hydrophobicity: 0.40
Percentage of hydrophilic amino acid: 28.30%
Percentage of hydrophobic amino acid: 71.70%
Ratio of %hydrophilic to %hydrophobic: 0.39

City	State	Year	Population	Area	Population Density	Area Density
Albany	NY	1990	20,000	100	200	200
Albany	NY	2000	22,000	100	220	220
Albany	NY	2010	24,000	100	240	240
Albany	NY	2020	26,000	100	260	260
Albany	NY	2030	28,000	100	280	280
Albany	NY	2040	30,000	100	300	300
Albany	NY	2050	32,000	100	320	320
Albany	NY	2060	34,000	100	340	340
Albany	NY	2070	36,000	100	360	360
Albany	NY	2080	38,000	100	380	380
Albany	NY	2090	40,000	100	400	400
Albany	NY	2100	42,000	100	420	420
Albany	NY	2110	44,000	100	440	440
Albany	NY	2120	46,000	100	460	460
Albany	NY	2130	48,000	100	480	480
Albany	NY	2140	50,000	100	500	500
Albany	NY	2150	52,000	100	520	520
Albany	NY	2160	54,000	100	540	540
Albany	NY	2170	56,000	100	560	560
Albany	NY	2180	58,000	100	580	580
Albany	NY	2190	60,000	100	600	600
Albany	NY	2200	62,000	100	620	620
Albany	NY	2210	64,000	100	640	640
Albany	NY	2220	66,000	100	660	660
Albany	NY	2230	68,000	100	680	680
Albany	NY	2240	70,000	100	700	700
Albany	NY	2250	72,000	100	720	720
Albany	NY	2260	74,000	100	740	740
Albany	NY	2270	76,000	100	760	760
Albany	NY	2280	78,000	100	780	780
Albany	NY	2290	80,000	100	800	800
Albany	NY	2300	82,000	100	820	820
Albany	NY	2310	84,000	100	840	840
Albany	NY	2320	86,000	100	860	860
Albany	NY	2330	88,000	100	880	880
Albany	NY	2340	90,000	100	900	900
Albany	NY	2350	92,000	100	920	920
Albany	NY	2360	94,000	100	940	940
Albany	NY	2370	96,000	100	960	960
Albany	NY	2380	98,000	100	980	980
Albany	NY	2390	100,000	100	1000	1000
Albany	NY	2400	102,000	100	1020	1020
Albany	NY	2410	104,000	100	1040	1040
Albany	NY	2420	106,000	100	1060	1060
Albany	NY	2430	108,000	100	1080	1080
Albany	NY	2440	110,000	100	1100	1100
Albany	NY	2450	112,000	100	1120	1120
Albany	NY	2460	114,000	100	1140	1140
Albany	NY	2470	116,000	100	1160	1160
Albany	NY	2480	118,000	100	1180	1180
Albany	NY	2490	120,000	100	1200	1200
Albany	NY	2500	122,000	100	1220	1220
Albany	NY	2510	124,000	100	1240	1240
Albany	NY	2520	126,000	100	1260	1260
Albany	NY	2530	128,000	100	1280	1280
Albany	NY					

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34393 atggtaaccaaagaatttttaaaaactaaacttgagtgttcagat
1   M V T K E F L K T K L E C S D
34438 atgtacgctcagaaaactcatagatgaggcacagggcgatgaaaat
16  M Y A Q K L I D E A Q G D E N
34483 aggttgtagcagcctattttatccaaaaacttgcagaacgtcataca
31  R L Y D L F I Q K L A E R H T
34528 cgccccgctatcgctcgaatattaa 34551
46  R P A I V E Y *

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Physico-chemical parameters of ORF 77ORF104

1 MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY

Number of amino acids: 52
 Average molecular weight (Daltons): 6193.13
 Mean amino acid weight (Daltons): 119.10
 Monoisotopic molecular weight (Daltons): 6189.12
 Mean amino acid monoisotopic weight (Daltons): 119.02

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	4	7.69%	7.58%	Cys	C	1	1.92%	1.66%
Asp	D	4	7.69%	5.28%	Glu	E	6	11.54%	6.37%
Phe	F	2	3.85%	4.09%	Gly	G	1	1.92%	6.84%
His	H	1	1.92%	2.24%	Ile	I	3	5.77%	5.81%
Lys	K	5	9.62%	5.95%	Leu	L	6	11.54%	9.42%
Met	M	2	3.85%	2.37%	Asn	N	1	1.92%	4.45%
Pro	P	1	1.92%	4.9%	Gln	Q	3	5.77%	3.97%
Arg	R	3	5.77%	5.16%	Ser	S	1	1.92%	7.12%
Thr	T	3	5.77%	5.67%	Val	V	2	3.85%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	3	5.77%	3.18%

Number of acidic (negative) amino acids (ED): 10 19.23%
 Number of basic (positive) amino acids (KR): 8 15.38%
 Total charge (KRED): 18 34.62%
 Net charge (KR - ED): -2 -3.85%
 Theoretical pI: 5.03
 Total linear charge density: 0.38
 Average hydrophobicity: -5.81
 Ratio of hydrophilicity to hydrophobicity: 1.47
 Percentage of hydrophilic amino acid: 53.85%
 Percentage of hydrophobic amino acid: 46.15%
 Ratio of %hydrophilic to %hydrophobic: 1.17

[illegible]

29268 atgttcaatataaaacgaaaaacggaggaagtcaagatgtattac
1 M F N I K R K T E E V K M Y Y
29313 gaaataggcgaaatcatacgaaaaatattcatgttaacggattc
16 E I G E I I R K N I H V N G F
29358 gattttaagctattcattttaaaagggtcatatgggcatatcaata
31 D F K L F I L K G H M G I S I
29403 caagttaaagatatgaacaacgtaccaattaaacatgcttatgtc
46 Q V K D M N N V P I K H A Y V
29448 gtatagtgagaatgacttagatatggcatcagacttatttaaccaa
61 V D E N D L D M A S D L F N Q
29493 gcaatagatgaatggattgaagagaacacagacgaacaggacaga
76 A I D E W I E E N T D E Q D R
29538 ctaattaacttagtcatgaaatggtag 29564
91 L I N L V M K W *

Physico-chemical parameters of ORF 77ORF182

1 MFNIKRKTEE VKMYYEIGEI IRKNIHVNGF DFKLFILKGH MGISIQVKDM NNVPIKHAYV
61 VDENDLDMAS DLFNQAIDEW IEENTDEQDR LINLVMKW

Number of amino acids: 98
Average molecular weight (Daltons): 11691.50
Mean amino acid weight (Daltons): 119.30
Monoisotopic molecular weight (Daltons): 11683.84
Mean amino acid monoisotopic weight (Daltons): 119.22

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	3	3.06%	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	9.18%	5.28%	Glu	E	9	9.18%	6.37%
Phe	F	5	5.10%	4.09%	Gly	G	4	4.08%	6.84%
His	H	3	3.06%	2.24%	Ile	I	12	12.24%	5.81%
Lys	K	9	9.18%	5.95%	Leu	L	6	6.12%	9.42%
Met	M	6	6.12%	2.37%	Asn	N	9	9.18%	4.45%
Pro	P	1	1.02%	4.9%	Gln	Q	3	3.06%	3.97%
Arg	R	3	3.06%	5.16%	Ser	S	2	2.04%	7.12%
Thr	T	2	2.04%	5.67%	Val	V	7	7.14%	6.58%
Trp	W	2	2.04%	1.23%	Tyr	Y	3	3.06%	3.18%

Number of acidic (negative) amino acids (ED): 18 18.37%
Number of basic (positive) amino acids (KR): 12 12.24%
Total charge (KRED): 30 30.61%
Net charge (KR - ED): -6 -6.12%
Theoretical pI: 4.76
Total linear charge density: 0.33
Average hydrophobicity: -3.89
Ratio of hydrophilicity to hydrophobicity: 1.28
Percentage of hydrophilic amino acid: 51.02%
Percentage of hydrophobic amino acid: 48.98%
Ratio of %hydrophilic to %hydrophobic: 1.04

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100017|lan|77ORF017 Phage 77 ORF |23269-23982|-3
(237 letters)

Database: nr

393,678 sequences; 120,452,765 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 4493986 emb CAB39045.1 (AL034559) predicted using hexExon; ...	41	0.010
gi 730607 sp P23250 RP11_YEAST NEGATIVE RAS PROTEIN REGULATOR P...	38	0.053
gi 3097044 emb CAA75299 (Y15035) K1R [Cowpox virus]	38	0.090
gi 2146245 pir S73794 hypothetical protein H91_orf180 - Mycopl...	38	0.090
gi 83910 pir S04682 ribosomal protein var1 - yeast (Candida gl...	37	0.15
gi 133135 sp P21358 RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN ...	37	0.15
gi 2128843 pir H64475 hypothetical protein MJ1409 - Methanococ...	36	0.20
gi 5107017 gb AAD39926.1 AF126285_2 (AF126285) RNA polymerase [...	36	0.35
gi 2146210 pir S73342 hypothetical protein E07_orf166 - Mycopl...	35	0.60

Database: swissprot

79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:			Score (bits)	E Value
sp P23250	RPI1_YEAST	NEGATIVE RAS PROTEIN REGULATOR PROTEIN.	38	0.014
sp P21358	RMAR_CANGA	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.	37	0.040
sp Q21444	LDLC_CAEEL	LDLC PROTEIN HOMOLOG.	34	0.35
sp P27240	RFAY_ECOLI	LIPOLYLSACCHARIDE CORE BIOSYNTHESIS PROT...	33	0.46
sp P53192	YGC0_YEAST	HYPOTHETICAL 27.1 KD PROTEIN IN ALK1-CKB1...	33	0.60
sp P32908	SMC1_YEAST	CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-B...	33	0.60
sp P54683	TAGB_DICDI	PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR ...	32	0.78
sp Q03100	CYAA_DICDI	ADENYLATE CYCLASE, AGGREGATION SPECIFIC (...)	32	0.78

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)
Algeria	1980	10.0	4.0	40.0
Algeria	1985	10.5	4.5	42.9
Algeria	1990	11.0	5.0	45.5
Algeria	1995	11.5	5.5	47.8
Algeria	2000	12.0	6.0	50.0
Algeria	2005	12.5	6.5	52.0
Algeria	2010	13.0	7.0	53.8
Algeria	2015	13.5	7.5	55.6
Algeria	2020	14.0	8.0	57.1
Algeria	2025	14.5	8.5	58.6
Algeria	2030	15.0	9.0	60.0
Algeria	2035	15.5	9.5	61.3
Algeria	2040	16.0	10.0	62.5
Algeria	2045	16.5	10.5	63.6
Algeria	2050	17.0	11.0	64.7
Algeria	2055	17.5	11.5	65.7
Algeria	2060	18.0	12.0	66.7
Algeria	2065	18.5	12.5	67.6
Algeria	2070	19.0	13.0	68.4
Algeria	2075	19.5	13.5	69.2
Algeria	2080	20.0	14.0	70.0
Algeria	2085	20.5	14.5	70.7
Algeria	2090	21.0	15.0	71.4
Algeria	2095	21.5	15.5	72.1
Algeria	2100	22.0	16.0	72.7
Algeria	2105	22.5	16.5	73.3
Algeria	2110	23.0	17.0	73.9
Algeria	2115	23.5	17.5	74.5
Algeria	2120	24.0	18.0	75.0
Algeria	2125	24.5	18.5	75.5
Algeria	2130	25.0	19.0	76.0
Algeria	2135	25.5	19.5	76.5
Algeria	2140	26.0	20.0	76.9
Algeria	2145	26.5	20.5	77.3
Algeria	2150	27.0	21.0	77.8
Algeria	2155	27.5	21.5	78.2
Algeria	2160	28.0	22.0	78.6
Algeria	2165	28.5	22.5	78.9
Algeria	2170	29.0	23.0	79.3
Algeria	2175	29.5	23.5	79.7
Algeria	2180	30.0	24.0	80.0
Algeria	2185	30.5	24.5	80.3
Algeria	2190	31.0	25.0	80.6
Algeria	2195	31.5	25.5	81.0
Algeria	2200	32.0	26.0	81.3
Algeria	2205	32.5	26.5	81.6
Algeria	2210	33.0	27.0	81.8
Algeria	2215	33.5	27.5	82.1
Algeria	2220	34.0	28.0	82.4
Algeria	2225	34.5	28.5	82.6
Algeria	2230	35.0	29.0	82.9
Algeria	2235	35.5	29.5	83.1
Algeria	2240	36.0	30.0	83.3
Algeria	2245	36.5	30.5	83.6
Algeria	2250	37.0	31.0	83.8
Algeria	2255	37.5	31.5	84.0
Algeria	2260	38.0	32.0	84.2
Algeria	2265	38.5	32.5	84.4
Algeria	2270	39.0	33.0	84.6
Algeria	2275	39.5	33.5	84.8
Algeria	2280	40.0	34.0	85.0
Algeria	2285	40.5	34.5	85.2
Algeria	2290	41.0	35.0	85.4
Algeria	2295	41.5	35.5	85.6
Algeria	2300	42.0	36.0	85.7
Algeria	2305	42.5	36.5	85.9
Algeria	2310	43.0	37.0	86.0
Algeria	2315	43.5	37.5	86.2
Algeria	2320	44.0	38.0	86.4
Algeria	2325	44.5	38.5	86.5
Algeria	2330	45.0	39.0	86.7
Algeria	2335	45.5	39.5	86.8
Algeria</				

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100019|lan|77ORF019 Phage 77 ORF|39851-40501|2
(216 letters)

Database: nr

373,355 sequences; 114,214,446 total letters

Sequences producing significant alignments:	Score	E
Value	(bits)	
gi 3341966 dbj BAA31932 (AB009866) orf 59 [bacteriophage phi PVL]	437	e-122
gi 2689911 (AE000792) B. burgdorferi predicted coding region BB...	38	0.058
gi 1171589 emb CAA64574 (X95275) frameshift [Plasmodium falcip...	37	0.10
gi 4493986 emb CAB39045.1 (AL034559) predicted using hexExon; ...	36	0.23
gi 141257 sp P18019 YPI9_CLOPE HYPOTHETICAL 14.5 KD PROTEIN (OR...	36	0.29
gi 133412 sp P27059 RPOB_ASTLO DNA-DIRECTED RNA POLYMERASE BETA...	35	0.51
gi 3122231 sp Q58851 HISX_METJA HISTIDINOL DEHYDROGENASE (HDH) ...	35	0.51
gi 3649757 emb CAB11106.1 (Z98547) predicted using hexExon; MA...	34	0.66
gi 2688313 (AE001146) sensory transduction histidine kinase, pu...	34	0.87

Database: swissprot

79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:	Score	E
Value	(bits)	
sp P18019 YPI9_CLOPE HYPOTHETICAL 14.5 KD PROTEIN (ORF9).	36	0.079
sp Q58851 HISX_METJA HISTIDINOL DEHYDROGENASE (EC 1.1.1.23) (H...	35	0.14
sp P27059 RPOB_ASTLO DNA-DIRECTED RNA POLYMERASE BETA CHAIN (E...	35	0.14
sp Q02224 CENE_HUMAN CENTROMERIC PROTEIN E (CENP-E PROTEIN).	34	0.31
sp P04931 ARP_PLAFA ASPARAGINE-RICH PROTEIN (AG319) (ARP) (FRA...	33	0.53
sp P18011 IPAB_SHIFL 62 KD MEMBRANE ANTIGEN.	32	0.69
sp P18709 VTA2_XENLA VITELLOGENIN A2 PRECURSOR (VTG A2) [CONTA...	32	0.90
sp Q64409 CP3H_CAVPO CYTOCHROME P450 3A17 (EC 1.14.14.1) (CYPI...	32	0.90
sp P21358 RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.	32	0.90
sp Q03945 IPAB_SHIDY 62 KD MEMBRANE ANTIGEN.	32	1.2

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100043|lan|77ORF043 Phage 77 ORF|29304-29564|3
(86 letters)

Database: nr
373,355 sequences; 114,214,446 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 3341947 dbj BAA31913 (AB009866) orf 39 [bacteriophage phi PVL]	182	6e-46
gi 744518 prf 2014422A FKBP-rapamycin-associated protein (Homo...	32	0.84
gi 1169736 sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN...	32	0.84
gi 1169735 sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTE...	32	0.84
gi 3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa...	32	0.84
gi 3875402 emb CAA98122 (Z73906) cDNA EST EMBL:D64544 comes fr...	31	2.5
gi 1084792 pir S54091 hypothetical protein YPR070w - yeast (Sa...	30	4.2

Database: swissprot
79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) ...	32	0.24
sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R...	32	0.24
sp P34554 YNP1_CAEEL HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C...	28	3.5
sp Q24118 LIO_DROME LINOTTE PROTEIN.	28	3.5
sp P80034 ACH2_BOMMO ANTICHYMOTRYPSIN II (ACHY-II).	28	3.5
sp P22922 A1AT_BOMMO ANTITRYPSIN PRECURSOR (AT).	28	3.5
sp Q44363 TRAA_AGRT6 CONJUGAL TRANSFER PROTEIN TRAA.	28	3.5
sp P38255 YBU5_YEAST HYPOTHETICAL 51.3 KD PROTEIN IN PHO5-VPS1...	27	6.0
sp P55822 SH3B_HUMAN SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PRO...	27	7.9
sp Q58482 YA82_METJA HYPOTHETICAL PROTEIN MJ1082.	27	7.9
sp P34252 YKK8_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN HAP4-AAT1...	27	7.9

[illegible]

1

—

2

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|122748|lan|77ORF182 Phage 77 ORF|29268-29564|3
(98 letters)

Database: nr
393,678 sequences; 120,452,765 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 3341947 dbj BAA31913.1 (AB009866) orf 39 [bacteriophage phi...	182	8e-46
gi 1084792 pir S54091 hypothetical protein YPR070w - yeast (Sa...	35	0.13
gi 1169736 sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN...	32	1.1
gi 744518 prf 2014422A FKBP-rapamycin-associated protein [Homo...	32	1.1
gi 5051381 emb CAB44736.1 (AL049653) dJ647M16.2 (FK506 binding...	32	1.1
gi 4826730 ref NP_004949.1 pFRAP1 FK506 binding protein 12-rap...	32	1.1
gi 3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa...	32	1.1

Database: swissprot
79,909 sequences; 29,054,478 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) ...	32	0.29
sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R...	32	0.29
sp P40557 YIA5_YEAST PUTATIVE DISULFIDE ISOMERASE YIL005W PREC...	29	3.3
sp Q24118 LIO_DROME LINOTTE PROTEIN.	28	4.4
sp Q44363 TRAA_AGRT6 CONJUGAL TRANSFER PROTEIN TRAA.	28	4.4
sp P80034 ACH2_BOMMO ANTICHYMOTRYPSIN II (ACHY-II).	28	4.4
sp P34554 YNP1_CAEEL HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C...	28	4.4
sp P22922 A1AT_BOMMO ANTITRYPSIN PRECURSOR (AT).	28	4.4

List of phage 77 ORFs that functionally tested

Table 5

1	77ORF005	48	77ORF052
2	77ORF006	49	77ORF053
3	77ORF007	50	77ORF054
4	77ORF008	51	77ORF055
5	77ORF009	52	77ORF058
6	77ORF010	53	77ORF059
7	77ORF011	54	77ORF064
8	77ORF012	55	77ORF065
9	77ORF013	56	77ORF066
10	77ORF014	57	77ORF069
11	77ORF015	58	77ORF070
12	77ORF016	59	77ORF071
13	77ORF017	60	77ORF072
14	77ORF018	61	77ORF073
15	77ORF019	62	77ORF074
16	77ORF020	63	77ORF075
17	77ORF021	64	77ORF077
18	77ORF022	65	77ORF079
19	77ORF023	66	77ORF080
20	77ORF024	67	77ORF085
21	77ORF025	68	77ORF092
22	77ORF026	69	77ORF094
23	77ORF027	70	77ORF096
24	77ORF028	71	77ORF098
25	77ORF029	72	77ORF102
26	77ORF030	73	77ORF104
27	77ORF031	74	77ORF109
28	77ORF032	75	77ORF112
29	77ORF033	76	77ORF117
30	77ORF034	77	77ORF118
31	77ORF035	78	77ORF120
32	77ORF036	79	77ORF124
33	77ORF037	80	77ORF128
34	77ORF038	81	77ORF130
35	77ORF039	82	77ORF133
36	77ORF040	83	77ORF140
37	77ORF041	84	77ORF147
38	77ORF042	85	77ORF149
39	77ORF043	86	77ORF151
40	77ORF044	87	77ORF155
41	77ORF045	88	77ORF157
42	77ORF046	89	77ORF167
43	77ORF047	90	77ORF175
44	77ORF048	91	77ORF176
45	77ORF049	92	77ORF178
46	77ORF050	93	77ORF179
47	77ORF051		

Table 6

NCBI Entrez Nucleotide QUERY BLAST Entrez

Details

staphylococcus aureus [Organism]

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citations 1-50 displayed (out of 558 found), page 1 of 12

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GenBank report



for the articles selected (default all).

☐ U77328

Staphylococcus aureus staphylokinase gene, partial cds

gi|2605637|gb|U77328.1|SAU77328 [2605637]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), [1 protein link](#), or [13 nucleotide neighbors](#))☐ AF151117

Staphylococcus aureus plasmid pKH3, complete sequence

gi|5031412|gb|AF151117.1|AF151117 [5031412]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [1 protein link](#))☐ AF151218

Staphylococcus aureus ribonuclease P RNA gene, complete sequence

gi|4929536|gb|AF151218.1|AF151218 [4929536]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), or [Graphical view](#))☐ AF146368

Staphylococcus aureus 16S ribosomal RNA gene, partial sequence

gi|4929362|gb|AF146368.1|AF146368 [4929362]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), or [Graphical view](#))☐ AF144661

Staphylococcus aureus subsp. anaerobius factor essential for methicillin resistance (femA) gene, complete cds

gi|4929298|gb|AF144661.1|AF144661 [4929298]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [1 protein link](#))☐ AF132117

Staphylococcus aureus ferrichrome uptake operon, complete sequence and unknown genes

gi|4928288|gb|AF132117.1|AF132117 [4928288]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [7 protein links](#))☐ Y15477

Staphylococcus aureus argI, glmM genes and ORF1 and ORF2

gi|3892891|emb|Y15477.1|SAARGFEMD [3892891]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), [4 protein links](#), or [4 nucleotide neighbors](#))

- ☐ Y09928
S.aureus CTORF1365, partial
gi|4775550|emb|Y09928.1|SACTORF13 [4775550]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [1 protein link](#))
- ☐ Y09594
S.aureus arg gene
gi|4775541|emb|Y09594.1|SAARG [4775541]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [2 protein links](#), or [5 nucleotide neighbors](#))
- ☐ AF134905
Staphylococcus aureus plasmid pRW001 CadD (cadD) gene, complete cds
gi|4680369|gb|AF134905.1|AF134905 [4680369]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [1 protein link](#))
- ☐ AB019536
Staphylococcus aureus norA23 gene for NorA, complete cds
gi|4115706|dbj|AB019536.1|AB019536 [4115706]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), [1 protein link](#), or [2 nucleotide neighbors](#))
- ☐ AJ237696
Staphylococcus aureus fus gene
gi|4582215|emb|AJ237696.1|SAU237696 [4582215]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [1 protein link](#))
- ☐ AF106851
Staphylococcus aureus LytN (lytN) and FmhC (fmhC) genes, complete cds
gi|4574236|gb|AF106851.1|AF106851 [4574236]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [2 protein links](#))
- ☐ AF106850
Staphylococcus aureus FmhB (fmhB) gene, complete cds
gi|4574234|gb|AF106850.1|AF106850 [4574234]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))
- ☐ AF106849
Staphylococcus aureus FmhA (fmhA) gene, complete cds
gi|4574232|gb|AF106849.1|AF106849 [4574232]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))
- ☐ M26321
Staphylococcus aureus plasmid pT181 repC gene, partial cds
gi|151689|gb|M26321.1|PT1REPC [151689]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), [1](#)

protein link, or 10 nucleotide neighbors)

☐ AF060191

Staphylococcus aureus strain ATCC27664 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558749|gb|AF060191.1|AF060191 [4558749]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060190

Staphylococcus aureus strain ATCC19095 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558747|gb|AF060190.1|AF060190 [4558747]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060189

Staphylococcus aureus strain ATCC14458 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558745|gb|AF060189.1|AF060189 [4558745]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060188

Staphylococcus aureus strain ATCC13565 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558743|gb|AF060188.1|AF060188 [4558743]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060187

Staphylococcus aureus strain ATCC10832 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558741|gb|AF060187.1|AF060187 [4558741]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060186

Staphylococcus aureus strain ATCC12598 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558739|gb|AF060186.1|AF060186 [4558739]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060185

Staphylococcus aureus strain ATCC25178 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558737|gb|AF060185.1|AF060185 [4558737]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

☐ AF060184

Staphylococcus aureus strain ATCC27217 heat shock protein 60 kDa (hsp60) gene, partial cds
gi|4558735|gb|AF060184.1|AF060184 [4558735]

(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))

- ☐ AF036324
Staphylococcus aureus subsp. aureus heat shock protein 60 (GroEL) gene, partial cds
gi|4558705|gb|AF036324.1| [4558705]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))
- ☐ AF036323
Staphylococcus aureus subsp. anaerobius heat shock protein 60 (GroEL) gene, partial cds
gi|4558703|gb|AF036323.1|AF036323 [4558703]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))
- ☐ AF053568
Staphylococcus aureus ATCC 25923 heat shock protein 60 gene, partial cds
gi|4205742|gb|AF053568.1|AF053568 [4205742]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), or [1 protein link](#))
- ☐ AJ132841
Staphylococcus aureus mapN gene
gi|4454323|emb|AJ132841.1|SAU132841 [4454323]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 protein link](#), or [2 nucleotide neighbors](#))
- ☐ Y13766
Staphylococcus aureus pnpA gene
gi|3970796|emb|Y13766.1|SAPNPA [3970796]
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- ☐ AF101234
Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene
gi|4530239|gb|AF101234.1|AF101234 [4530239]
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- ☐ AJ133520
Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes)
gi|4490611|emb|AJ133520.1|SAU133520 [4490611]
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- ☐ AJ133495
Staphylococcus aureus ribonucleotide reductase operon
gi|4490607|emb|AJ133495.1|SAU133495 [4490607]
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- ☐ AJ132803
Staphylococcus aureus ORF1 and ORF2 (partial)

gi|4454320|emb|AJ132803.1|SAU132803 [4454320]

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☐ AB016487

Staphylococcus aureus gene for enterotoxin type Gv, complete cds

gi|4126682|dbj|AB016487.1|AB016487 [4126682]

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☐ AB016431

Staphylococcus aureus, zinc responsible operon *czr* genes, complete and partial cds

gi|4126670|dbj|AB016431.1|AB016431 [4126670]

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☐ AB015981

Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds

gi|4001723|dbj|AB015981.1|AB015981 [4001723]

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☐ AB015195

Staphylococcus aureus gene for LytN and Ephr, complete cds

gi|3767591|dbj|AB015195.1|AB015195 [3767591]

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☐ AF107307

Staphylococcus aureus subsp. anaerobius 16S ribosomal RNA gene, partial sequence

gi|4406286|gb|AF107307.1|AF107307 [4406286]

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☐ AF079518

Staphylococcus aureus lipoprotein SirA (*sirA*), SirB (*sirB*), and SirC (*sirC*) genes, complete cds

gi|3694941|gb|AF079518.1|AF079518 [3694941]

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☐ AJ223806

Staphylococcus aureus map gene, partial

gi|4138455|emb|AJ223806.1|SAU223806 [4138455]

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☐ Y18018

Staphylococcus aureus plasmid pSES30 including *ermC* gene, partial

gi|4138444|emb|Y18018.1|SAU18018 [4138444]

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- ☐ Y17795
Staphylococcus aureus prfA, pbp2 genes
gi|3955029|emb|Y17795.1|SAU17795 [3955029]
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- ☐ AJ005647
Staphylococcus aureus sdrE gene
gi|3550595|emb|AJ005647.1|SAU5647 [3550595]
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- ☐ AJ005646
Staphylococcus aureus sdrD gene
gi|3550593|emb|AJ005646.1|SAU5646 [3550593]
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- ☐ AJ005645
Staphylococcus aureus sdrC gene
gi|3550591|emb|AJ005645.1|SAU5645 [3550591]
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- ☐ V01282
Staphylococcus aureus plasmid pSN2 Includes an unknown gene
gi|46653|emb|V01282.1|SAPSN2 [46653]
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- ☐ AF121672
Staphylococcus aureus superoxide dismutase SodA (sodA) gene, complete cds
gi|4325246|gb|AF121672.1|AF121672 [4325246]
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- ☐ AF072726
Staphylococcus aureus putative heme A synthase (ctaA) gene, complete cds
gi|3320605|gb|AF072726.1|AF072726 [3320605]
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- ☐ AF115379
Staphylococcus aureus surface protein Pls (pls) gene, complete cds
gi|4185564|gb|AF115379.1|AF115379 [4185564]
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- ☐ AF034153
Staphylococcus aureus phospho-N-acetylmuramoyl-pentapeptide translocase (mraY) gene,

complete cds

gi|4104229|gb|AF034153.1|AF034153 [4104229]

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- ☐ AF029244
Staphylococcus aureus 60 kDa heat shock protein (hsp60) gene, partial cds
gi|4103899|gb|AF029244.1|AF029244 [4103899]
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 - ☐ U67965
Staphylococcus aureus lytic regulatory protein gene, complete cds
gi|4097756|gb|U67965.1|SAU67965 [4097756]
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 - ☐ U96610
Staphylococcus aureus plasmid pSK6, complete genome
gi|4090653|gb|U96610.1|SAU96610 [4090653]
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 - ☐ U96609
Staphylococcus aureus plasmid pSK3, complete genome
gi|4090650|gb|U96609.1|SAU96609 [4090650]
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 - ☐ U73027
Staphylococcus aureus transposon Tn5405 unknown gene, complete cds
gi|2811117|gb|U73027.1|SAU73027 [2811117]
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 - ☐ U73026
Staphylococcus aureus transposon Tn5405 streptothricine-acetyl-transferase (sat4) pseudogene, complete sequence
gi|2811116|gb|U73026.1|SAU73026 [2811116]
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 - ☐ U73025

Staphylococcus aureus transposon Tn5405 unknown gene, complete cds

gi|2811114|gb|U73025.1|SAU73025 [2811114]

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☐ AF068904

Staphylococcus aureus cell division protein FtsZ (ftsZ) gene, partial cds; YlmD (ylmD), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), and YlmH (ylmH) genes, complete cds; and cell division protein DivIVA (divIVA) gene, partial cds

gi|4009490|gb|AF068904.1|AF068904 [4009490]

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☐ U60050

Staphylococcus aureus major cold-shock protein (cspA) gene, partial cds

gi|1402770|gb|U60050.1|SAU60050 [1402770]

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☐ D10907

Staphylococcus aureus insertion element IS431, partial sequence, clone:MR108-4

gi|216973|dbj|D10907.1|STAIS431B [216973]

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☐ D10906

Staphylococcus aureus insertion element IS431, partial sequence, clone:MR108-3

gi|216972|dbj|D10906.1|STAIS431A [216972]

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☐ AF053140

Staphylococcus aureus plasmid pIB485 enterotoxin D (sed) gene, partial cds; and enterotoxin J (sej) gene, complete cds

gi|3372540|gb|AF053140.1|AF053140 [3372540]

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☐ AB013298

Staphylococcus aureus genes for leader peptide, MsrSA and MphBM, complete cds

gi|3892641|dbj|AB013298.1|AB013298 [3892641]

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☐ Y16431

Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4 ORF's

gi|3850845|emb|Y16431.1|SAU16431 [3850845]

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☐ AF076684

6090749320460

Staphylococcus aureus oligopeptide transporter putative membrane permease domain (opp-2B), oligopeptide transporter putative membrane permease domain (opp-2C), oligopeptide transporter putative ATPase domain (opp-2D), and oligopeptide transporter putative ATPase domain (opp-2F) genes, complete cds
gi|3800824|gb|AF076684.1|AF076684 [3800824]
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☐ AF076683

Staphylococcus aureus oligopeptide transporter putative substrate binding domain (opp-1A), oligopeptide transporter putative membrane permease domain (opp-1B), oligopeptide transporter putative membrane permease domain (opp-1C), oligopeptide transporter putative ATPase domain (opp-1D), and oligopeptide transporter putative ATPase domain (opp-1F) genes, complete cds; and unknown gene
gi|3800817|gb|AF076683.1|AF076683 [3800817]
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☐ Y13225

Staphylococcus aureus lukE, lukD genes
gi|2765302|emb|Y13225.1|SALUKED [2765302]
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☐ AF094826

Staphylococcus aureus novel exotoxins gene cluster, complete sequence; and HsdM-like protein gene, partial cds
gi|3806103|gb|AF094826.1|AF094826 [3806103]
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☐ AJ223480

Staphylococcus aureus trxA and uvrC genes and partial mutS and dhsC genes
gi|3776109|emb|AJ223480.1|SATRXA [3776109]
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☐ AF093548

Staphylococcus aureus tyrosine recombinase XerD (xerD) gene, complete cds
gi|3747041|gb|AF093548.1|AF093548 [3747041]
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☐ AJ005352

Staphylococcus aureus, Sst putative iron transport operon
gi|3724154|emb|AJ005352.1|SAA005352 [3724154]
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☐ AF051916

Staphylococcus aureus plasmid pJE1 remnant of replication protein Rep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylate synthetase ThyE (thyE), and putative transposase Tnp (tnp) genes, complete cds; and unknown gene
gi|3676404|gb|AF051916.1|AF051916 [3676404]
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protein links, or 22 nucleotide neighbors)

☐ Y09927

S.aureus glmM gene

gi|1729788|emb|Y09927.1|SAURED [1729788]

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☐ AF051917

Staphylococcus aureus plasmid pSK41, complete sequence

gi|3676412|gb|AF051917.1|AF051917 [3676412]

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☐ S77058

bler=bleomycin-resistance gene [Staphylococcus aureus, MRSA, B-26, Genomic, 297 nt]

gi|913952|gb|S77058.1|S77058 [913952]

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☐ S65052

hlg2=gamma-hemolysin II...lukF=leukocidin F component [Staphylococcus aureus, MRSA No. 4, Genomic, 3 genes, 4353 nt]

gi|410004|gb|S65052.1|S65052 [410004]

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☐ AF009671

Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine : D-glutamate ligase (murD) gene, complete cds

gi|2305091|gb|AF009671.1|AF009671 [2305091]

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☐ U81973

Staphylococcus aureus capsule gene cluster Cap5A through Cap5P genes, complete cds

gi|1773339|gb|U81973.1|SAU81973 [1773339]

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☐ U77308

Staphylococcus aureus O-acetyl transferase (cap5H) gene, complete cds

gi|1673628|gb|U77308.1|SAU77308 [1673628]

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☐ U20869

Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds

gi|706919|gb|U20869.1|SAU20869 [706919]

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protein links, or 2 nucleotide neighbors)

☐ U89396

Staphylococcus aureus hemCDBL gene cluster: porphobilinogen deaminase (hemC), uroporphyrinogen III synthase (hemD), d-aminolevulinic acid dehydratase (hemB) and GSA-1-aminotransferase (hemL) genes, complete cds

gi|2589180|gb|U89396.1|SAU89396 [2589180]

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☐ U94706

Staphylococcus aureus strain ATCC 8325-4 cell wall/cell division gene cluster, yllB, yllC, yllD, pbpA, mraY, murD, div1B, ftsA and ftsZ genes, complete cds

gi|2149889|gb|U94706.1|SAU94706 [2149889]

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☐ U41072

Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds

gi|1314300|gb|U41072.1|SAU41072 [1314300]

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☐ U52961

Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds

gi|1841516|gb|U52961.1|SAU52961 [1841516]

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☐ U21636

Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds

gi|710420|gb|U21636.1|SAU21636 [710420]

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☐ U65000

Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds

gi|1595808|gb|U65000.1|SAU65000 [1595808]

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☐ U48826

Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds

gi|1397238|gb|U48826.1|SAU48826 [1397238]

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☐ U20503

Staphylococcus aureus MHC class II analog gene, complete cds

gi|1001960|gb|U20503.1|SAU20503 [1001960]

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- ☐ U11789
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV8 16S-23S rRNA spacer region
gi|6445560|gb|U11789.1|SAU11789 [644560]
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- ☐ U11788
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV7 16S-23S rRNA spacer region
gi|6445559|gb|U11788.1|SAU11788 [644559]
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- ☐ U11787
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV43 16S-23S rRNA spacer region
gi|6445558|gb|U11787.1|SAU11787 [644558]
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- ☐ U11786
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV42 16S-23S rRNA spacer region
gi|6445557|gb|U11786.1|SAU11786 [644557]
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- ☐ U11785
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV41 16S-23S rRNA spacer region
gi|6445556|gb|U11785.1|SAU11785 [644556]
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- ☐ U11784
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV40 16S-23S rRNA spacer region
gi|6445555|gb|U11784.1|SAU11784 [644555]
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- ☐ U11783
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV4 16S-23S rRNA spacer region
gi|6445554|gb|U11783.1|SAU11783 [644554]
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- ☐ U11782
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV38 16S-23S rRNA
spacer region
gi|644553|gb|U11782.1|SAU11782 [644553]
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- ☐ U11781
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV34 16S-23S rRNA
spacer region
gi|644552|gb|U11781.1|SAU11781 [644552]
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- ☐ U11780
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV32 16S-23S rRNA
spacer region
gi|644551|gb|U11780.1|SAU11780 [644551]
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- ☐ U11779
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 16S-23S rRNA
spacer region
gi|644550|gb|U11779.1|SAU11779 [644550]
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- ☐ U11778
Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV27 16S-23S rRNA
spacer region
gi|644549|gb|U11778.1|SAU11778 [644549]
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- ☐ U11777
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV2 16S-23S rRNA spacer region
gi|644548|gb|U11777.1|SAU11777 [644548]
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- ☐ U11776
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV17 16S-23S rRNA spacer region
gi|644547|gb|U11776.1|SAU11776 [644547]
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- ☐ U11775
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV13 16S-23S rRNA spacer region
gi|644546|gb|U11775.1|SAU11775 [644546]
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- ☐ U11774
Staphylococcus aureus methicillin-resistant isolate H11 clone RRNV12 16S-23S rRNA spacer region
gi|644545|gb|U11774.1|SAU11774 [644545]
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- ☐ U11773
Staphylococcus aureus methicillin-resistant isolate D46 clone RRN4 16S-23S rRNA spacer region
gi|644544|gb|U11773.1|SAU11773 [644544]
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- ☐ AF053772
Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds

gi|3327946|gb|AF053772.1|AF053772 [3327946]
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☐ AF053771

Staphylococcus aureus plasmid pSK156 transcriptional regulator QacR (qacR), multidrug efflux protein QacB, delta-orf186, and putative transposase TnpA (tnpA) genes, complete cds
gi|3327941|gb|AF053771.1|AF053771 [3327941]
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☐ AF029731

Staphylococcus aureus large conductance mechanosensitive channel (mscL) gene, complete cds
gi|3135291|gb|AF029731.1|AF029731 [3135291]
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☐ AF027155

Staphylococcus aureus IgG-binding protein SBI (sbi) gene, complete cds
gi|2827911|gb|AF027155.1|AF027155 [2827911]
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☐ AF024571

Staphylococcus aureus high affinity proline permease (putP) gene, complete cds
gi|2565310|gb|AF024571.1|AF024571 [2565310]
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☐ U87144

Staphylococcus aureus branched-chain amino acid carrier protein gene, complete cds
gi|2315994|gb|U87144.1|SAU87144 [2315994]
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☐ AF086644

Staphylococcus aureus type b beta-lactamase (blaZ) gene, partial cds
gi|3603440|gb|AF086644.1|AF086644 [3603440]
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☐ AJ223781

Staphylococcus aureus trxB gene
gi|4379427|emb|AJ223781.1|SAAJ3781 [4379427]
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☐ AF076030

Staphylococcus aureus 16S ribosomal RNA gene, partial sequence
gi|3551854|gb|AF076030.1|AF076030 [3551854]
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neighbors)

- ☐ AF044951
Staphylococcus aureus repressor protein (rzcA) and transport protein (rzcB) genes, complete cds
gi|3445565|gb|AF044951.1|AF044951 [3445565]
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 - ☐ AF044906
Staphylococcus aureus isolate SA92 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411113|gb|AF044906.1|AF044906 [3411113]
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 - ☐ AF044905
Staphylococcus aureus isolate SA32 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411111|gb|AF044905.1|AF044905 [3411111]
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 - ☐ AF044904
Staphylococcus aureus isolate SA22 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411109|gb|AF044904.1|AF044904 [3411109]
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 - ☐ AF044903
Staphylococcus aureus isolate SA198 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411107|gb|AF044903.1|AF044903 [3411107]
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 - ☐ AF044902
Staphylococcus aureus isolate SA85 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411105|gb|AF044902.1|AF044902 [3411105]
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 - ☐ AF044901
Staphylococcus aureus isolate SA76 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411103|gb|AF044901.1|AF044901 [3411103]
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 - ☐ AF044900
Staphylococcus aureus isolate SA75 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411101|gb|AF044900.1|AF044900 [3411101]
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- ☐ AF044899
Staphylococcus aureus isolate R155 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411099|gb|AF044899.1|AF044899 [3411099]
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- ☐ AF044898
Staphylococcus aureus isolate SAM1 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411097|gb|AF044898.1|AF044898 [3411097]
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- ☐ AF044897
Staphylococcus aureus isolate SA74 DNA topoisomerase IV subunit A (grlA) gene, partial cds
gi|3411095|gb|AF044897.1|AF044897 [3411095]
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- ☐ AF044075
Staphylococcus aureus isolate sa92 DNA gyrase subunit A (gyrA) gene, partial cds
gi|3411091|gb|AF044075.1|AF044075 [3411091]
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- ☐ AF044074
Staphylococcus aureus isolate sa32 DNA gyrase subunit A (gyrA) gene, partial cds
gi|3411089|gb|AF044074.1|AF044074 [3411089]
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- ☐ AF044073
Staphylococcus aureus isolate sa22 DNA gyrase subunit A (gyrA) gene, partial cds
gi|3411087|gb|AF044073.1|AF044073 [3411087]
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- ☐ AF044072
Staphylococcus aureus isolate sa198 DNA gyrase subunit A (gyrA) gene, partial cds
gi|3411085|gb|AF044072.1|AF044072 [3411085]
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- ☐ AF044071
Staphylococcus aureus isolate sa85 DNA gyrase subunit A (gyrA) gene, partial cds
gi|3411083|gb|AF044071.1|AF044071 [3411083]
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3411099 3411097 3411095 3411091 3411089 3411087 3411085 3411083

- [illegible]

gi|3323612|gb|AF064774.1|AF064774 [3323612]

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□ AF064773

Staphylococcus aureus extracellular enterotoxin type G precursor (SEG) gene, complete cds
gi|3323610|gb|AF064773.1|AF064773 [3323610]

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Y14370

Staphylococcus aureus RF3, murE, ypfP genes

gi|3256221|emb|Y14370.1|SAY14370 [3256221]

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□ AF065394

Staphylococcus aureus enolase (eno) gene, complete cds

gi|3152724|gb|AF065394.1|AF065394 [3152724]

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□ AF062376

Staphylococcus aureus strain E3452, unidentified sequence 2

gi|3142435|gb|AF062376.1|AF062376 [3142435]

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AF062375

Staphylococcus aureus strain E3452; unidentified sequence 1

gi|3142434|gb|AF062375.1|AF062375 [3142434]

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AF062374

Staphylococcus aureus strain W6652, unidentified sequence 2

gi|3142433|gb|AF062374.1|AF062374 [3142433]

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□ AF062373

Staphylococcus aureus strain W6652, unidentified sequence 1

gi|3142432|gb|AF062373.1|AF062373 [3142432]

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☐ AB007500

Staphylococcus aureus genes for penicillin-binding protein 1, MraY, MurD, partial and complete cds

gi|2463558|dbj|AB007500.1|AB007500 [2463558]

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☐ Y09924

S.aureus serS gene

gi|1835217|emb|Y09924.1|SASERS [1835217]

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☐ U63529

Staphylococcus aureus novel antigen gene, complete cds

gi|1488694|gb|U63529.1|SAU63529 [1488694]

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☐ AF033191

Staphylococcus aureus strain ATCC25923 clone pSa-442 Sau3AI fragment

gi|2988485|gb|AF033191.1|AF033191 [2988485]

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Staphylococcus aureus 16S rRNA gene

gi|2950318|emb|Y15856.1|SAY15856 [2950318]

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Staphylococcus aureus recG gene, complete cds

gi|2826895|dbj|AB000439.1|AB000439 [2826895]

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Staphylococcus aureus coenzyme A disulfide reductase gene, complete cds

gi|2792489|gb|AF041467.1|AF041467 [2792489]

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Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224

gi|2791983|emb|Y14051.1|SAMECAR1I [2791983]

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Staphylococcus aureus plasmid pIP1633 pristinamycin resistance protein VgaB (vgaB) gene, complete cds

gi|2769707|gb|U82085.1|SAU82085 [2769707]

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Staphylococcus aureus plasmid pIM51 signal transduction protein (agrB) gene, partial cds; pre-pheromone (agrD) and mutant sensor protein (agrC) genes, complete cds; and transducer protein (agrA) gene, partial cds

gi|2736224|gb|AF026122.1|AF026122 [2736224]

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☐ AF026121

Staphylococcus aureus plasmid pIM50 signal transduction protein (agrB) gene, partial cds; pre-pheromone (agrD) and mutant sensor protein (agrC) genes, complete cds; and transducer protein (agrA) gene, partial cds

gi|2736219|gb|AF026121.1|AF026121 [2736219]

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☐ AF026120

Staphylococcus aureus plasmid pIM49 signal transduction protein (agrB) gene, partial cds; pre-pheromone (agrD) and mutant sensor protein (agrC) genes, complete cds; and transducer protein (agrA) gene, partial cds

gi|2736214|gb|AF026120.1|AF026120 [2736214]

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☐ AB009635

Staphylococcus aureus DNA for Fmt, complete cds

gi|2696795|dbj|AB009635.1|AB009635 [2696795]

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☐ AB006796

Staphylococcus aureus genes for LukS-PV, LukF-PV and integrase, complete cds

gi|2696710|dbj|AB006796.1|AB006796 [2696710]

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☐ U39769

Staphylococcus aureus 16S-23S ribosomal RNA spacer region

gi|2668542|gb|U39769.1|SAU39769 [2668542]

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☐ D00184

Staphylococcus aureus gene for staphylocoagulase, complete cds

gi|216976|dbj|D00184.1|STASCAG [216976]

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☐ X56628

Staphylococcus aureus qacA gene for antiseptic resistance protein

gi|773395|emb|X56628.1|SAQACA [773395]

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☐ AF033018

Staphylococcus aureus ribosome recycling factor (frr) gene, complete cds

gi|2645712|gb|AF033018.1|AF033018 [2645712]

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- ☐ AF034076
Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase (murC) gene, complete cds
gi|2642658|gb|AF034076.1|AF034076 [2642658]
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- ☐ D82063
Staphylococcus aureus gene for lipophilic protein, partial cds
gi|2641997|dbj|D82063.1|D82063 [2641997]
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- ☐ D76414
Staphylococcus aureus gene for histidyl-tRNA synthetase, ppGpp hydrolase, lytic enzyme, complete cds
gi|2580431|dbj|D76414.1|D76414 [2580431]
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- ☐ U57060
Staphylococcus aureus scdA gene, complete cds
gi|1575060|gb|U57060.1|SAU57060 [1575060]
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- ☐ D89066
Staphylococcus aureus DNA for DnaA, complete cds
gi|1854450|dbj|D89066.1|D89066 [1854450]
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- ☐ U85095
Staphylococcus aureus strain KSI9051 agr signal transduction pathway genes: AgrB (agrB) gene, partial cds; pre-pheromone AgrD (agrD) and truncated sensor protein AgrC-31 (agrC) genes, complete cds; and transducer protein AgrA (agrA) gene, partial cds
gi|1916237|gb|U85095.1|SAU85095 [1916237]
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- ☐ U85097
Staphylococcus aureus strain RN4282 agr signal transduction pathway genes: AgrB (agrB) gene, partial cds, pre-pheromone AgrD (agrD) and sensor protein AgrC (agrC) genes, complete cds, and transducer protein AgrA (agrA) gene, partial cds
gi|1916245|gb|U85097.1|SAU85097 [1916245]
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- ☐ U85096
Staphylococcus aureus strain KSI54 agr signal transduction pathway genes: AgrB (agrB) gene, partial cds, pre-pheromone AgrD (agrD) and sensor protein AgrC (agrC) genes, complete cds,

and transducer protein AgrA (agrA) gene, partial cds

gi|1916241|gb|U85096.1|SAU85096 [1916241]

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☐ D42078

Staphylococcus aureus DNA for N-acetyl-glucosaminidase, partial cds

gi|2506026|dbj|D42078.1|D42078 [2506026]

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☐ AF015929

Staphylococcus aureus 16S ribosomal RNA gene, partial sequence

gi|2353761|gb|AF015929.1|AF015929 [2353761]

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☐ D10369

Staphylococcus aureus gene for glutamic acid-specific protease, partial cds

gi|2344764|dbj|D10369.1|D10369 [2344764]

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☐ A48955

Sequence 2 from Patent WO9604380

gi|2302593|emb|A48955.1|A48955 [2302593]

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☐ A48501

Sequence 3 from Patent WO9603516

gi|2302280|emb|A48501.1|A48501 [2302280]

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☐ A48500

Sequence 2 from Patent WO9603516

gi|2302278|emb|A48500.1|A48500 [2302278]

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☐ A48499

Sequence 1 from Patent WO9603516

gi|2302277|emb|A48499.1|A48499 [2302277]

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☐ A47600

Sequence 13 from Patent EP0688873

gi|2301548|emb|A47600.1|A47600 [2301548]

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- ☐ A47599
Sequence 12 from Patent EP0688873
gi|2301547|emb|A47599.1|A47599 [2301547]
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 - ☐ A47598
Sequence 11 from Patent EP0688873
gi|2301546|emb|A47598.1|A47598 [2301546]
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 - ☐ A47597
Sequence 10 from Patent EP0688873
gi|2301545|emb|A47597.1|A47597 [2301545]
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 - ☐ A47596
Sequence 9 from Patent EP0688873
gi|2301544|emb|A47596.1|A47596 [2301544]
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 - ☐ A47595
Sequence 8 from Patent EP0688873
gi|2301543|emb|A47595.1|A47595 [2301543]
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 - ☐ A47594
Sequence 7 from Patent EP0688873
gi|2301542|emb|A47594.1|A47594 [2301542]
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 - ☐ A44534
Sequence 10 from Patent WO9513395
gi|2299352|emb|A44534.1|A44534 [2299352]
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 - ☐ A44533
Sequence 9 from Patent WO9513395
gi|2299351|emb|A44533.1|A44533 [2299351]
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 - ☐ A44529
Sequence 5 from Patent WO9513395
gi|2299347|emb|A44529.1|A44529 [2299347]
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 - ☐ A44528
Sequence 4 from Patent WO9513395
gi|2299346|emb|A44528.1|A44528 [2299346]

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☐ A44527

Sequence 3 from Patent WO9513395

gi|2299345|emb|A44527.1|A44527 [2299345]

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☐ A44526

Sequence 2 from Patent WO9513395

gi|2299344|emb|A44526.1|A44526 [2299344]

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☐ A44525

Sequence 1 from Patent WO9513395

gi|2299343|emb|A44525.1|A44525 [2299343]

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☐ A39696

Sequence 9 from Patent WO9418327

gi|2295954|emb|A39696.1|A39696 [2295954]

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☐ AF001783

Staphylococcus aureus strain RN8462 AgrB (agrB), AgrD (agrD) and AgrC (agrC) genes, complete cds

gi|2258297|gb|AF001783.1|AF001783 [2258297]

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☐ AF001782

Staphylococcus aureus strain SA502A AgrB (agrB), AgrD (agrD) and AgrC (agrC) genes, complete cds

gi|2258293|gb|AF001782.1|AF001782 [2258293]

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☐ L77194

Staphylococcus aureus peptidoglycan hydrolase (lytM) gene, complete cds

gi|2239273|gb|L77194.1|STALYTM [2239273]

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☐ AF003593

Staphylococcus aureus CspC (cspC) gene, complete cds

gi|2226348|gb|AF003593.1|AF003593 [2226348]

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- ☐ X74219
S.aureus gene for isoleucyl-tRNA synthetase
gi|437915|emb|X74219.1|SAILES [437915]
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- ☐ Y10419
S.aureus gene encoding outer surface binding 70kD protein, partial
gi|2190506|emb|Y10419.1|SAOSB70KD [2190506]
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- ☐ M63177
S.aureus sigma factor (plaC) gene, complete cds
gi|153068|gb|M63177.1|STAPLAC [153068]
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- ☐ E08773
DNA encoding Protein A
gi|2176885|dbj|E08773.1|E08773 [2176885]
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- ☐ E07163
Partial sequence of Staphylococcus aureus
gi|2175310|dbj|E07163.1|E07163 [2175310]
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- ☐ E07162
Partial sequence of Staphylococcus aureus
gi|2175309|dbj|E07162.1|E07162 [2175309]
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- ☐ E07161
Partial sequence of Staphylococcus aureus
gi|2175308|dbj|E07161.1|E07161 [2175308]
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- ☐ E07160
Partial sequence of *Staphylococcus aureus*
gi|2175307|dbj|E07160.1|E07160 [2175307]
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- ☐ E07159
Partial sequence of *Staphylococcus aureus*
gi|2175306|dbj|E07159.1|E07159 [2175306]
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- ☐ E07158
Partial sequence of *Staphylococcus aureus*
gi|2175305|dbj|E07158.1|E07158 [2175305]
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- ☐ E07157
Partial sequence of *Staphylococcus aureus*
gi|2175304|dbj|E07157.1|E07157 [2175304]
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- ☐ E07156
Partial sequence of *Staphylococcus aureus*
gi|2175303|dbj|E07156.1|E07156 [2175303]
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- ☐ E07155
Partial sequence of *Staphylococcus aureus*
gi|2175302|dbj|E07155.1|E07155 [2175302]
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- ☐ E03836
DNA encoding V8 protease
gi|2172050|dbj|E03836.1|E03836 [2172050]
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- ☐ E03835
DNA encoding V8-like protease
gi|2172049|dbj|E03835.1|E03835 [2172049]
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- ☐ E03526
gDNA encoding protein A
gi|2171742|dbj|E03526.1|E03526 [2171742]
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- ☐ E02873
DNA encoding staphylokinase(SAK)
gi|2171098|dbj|E02873.1|E02873 [2171098]
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- ☐ E01690
Genomic DNA of protein A of staphylococcus aureus
gi|2169943|dbj|E01690.1|E01690 [2169943]
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- ☐ E00876
DNA fragment comprising a promoter of sak gene and the region coding the signal peptide
gi|2169137|dbj|E00876.1|E00876 [2169137]
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- ☐ E00203
DNA sequence of protein A-like molecule
gi|2168499|dbj|E00203.1|E00203 [2168499]
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- ☐ D83951
Staphylococcus aureus DNA for LukM component, LukF-PV like component, complete cds
gi|1230553|dbj|D83951.1|STALUK [1230553]
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- ☐ D17366
Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs
gi|643603|dbj|D17366.1|STAATLA [643603]
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- ☐ D42144
Staphylococcus aureus gene for LUKM, complete cds
gi|577648|dbj|D42144.1|STAPLUKM [577648]
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- ☐ D42143
Staphylococcus aureus hlg2 gene for gamma-hemolysin, complete cds
gi|577646|dbj|D42143.1|STAHLG2 [577646]
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- ☐ D10489
Staphylococcus aureus genes for DNA gyrase A and B, complete cds
gi|540540|dbj|D10489.1|STAGYRABA [540540]

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☐ D21131

Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds

gi|531264|dbj|D21131.1|STASRM551A [531264]

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☐ D30690

Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds

gi|487326|dbj|D30690.1|STANH5 [487326]

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☐ D14711

Staphylococcus aureus HSP10 and HSP60 genes

gi|441206|dbj|D14711.1|STAHSP [441206]

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☐ D90119

S. aureus norA gene

gi|216974|dbj|D90119.1|STANORA [216974]

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☐ D00730

S. aureus glutamic acid specific protease (EC 3.4.21.19) gene

gi|216970|dbj|D00730.1|STAGASP [216970]

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☐ D83357

Staphylococcus aureus (strain ATCC12600T) gene for 16S rRNA, partial sequence

gi|1199939|dbj|D83357.1|STA16SRR05 [1199939]

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☐ D83356

Staphylococcus aureus (strain OA1) gene for 16S rRNA, partial sequence

gi|1199938|dbj|D83356.1|STA16SRR04 [1199938]

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☐ D83355

Staphylococcus aureus (strain ATCC35844T) gene for 16S rRNA, partial sequence

gi|1199937|dbj|D83355.1|STA16SRR03 [1199937]

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- ☐ D83354
Staphylococcus aureus (strain Kitami) gene for 16S rRNA, partial sequence
gi|1199936|dbj|D83354.1|STA16SRR02 [1199936]
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- ☐ D83353
Staphylococcus aureus (strain FU16A2) gene for 16S rRNA, partial sequence
gi|1199935|dbj|D83353.1|STA16SRR01 [1199935]
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- ☐ D12572
Staphylococcus aureus rrmA gene for 23S ribosomal RNA
gi|216969|dbj|D12572.1|STA23SRNA [216969]
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- ☐ D86727
Staphylococcus aureus DNA for DNA polymerase III, complete cds
gi|1483181|dbj|D86727.1|D86727 [1483181]
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- ☐ D86240
Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds
gi|1405333|dbj|D86240.1|D86240 [1405333]
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- ☐ D67075
Staphylococcus aureus DNA for DNA topoisomerase IV GrlB subunit, DNA topoisomerase IV GrlA subunit, complete cds
gi|1777319|dbj|D67075.1|D67075 [1777319]
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- ☐ D67074
Staphylococcus aureus DNA for DNA topoisomerase IV GrlB subunit, DNA topoisomerase IV GrlA subunit, complete cds
gi|1777316|dbj|D67074.1|D67074 [1777316]
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- ☐ U97062
Staphylococcus aureus NCTC 8325 SecA (secA) gene, complete cds
gi|2078389|gb|U97062.1|SAU97062 [2078389]
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- ☐ U96620
Staphylococcus aureus NCTC 8325 ribosomal protein L30 (L30), ribosomal protein L15 (L15) and SecY (secY) genes, complete cds
gi|2078379|gb|U96620.1|SAU96620 [2078379]
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- ☐ U96619
Staphylococcus aureus NCTC 8325 SecE (secE), NusG (nusG) and RplK (rplK) genes, complete cds
gi|2078375|gb|U96619.1|SAU96619 [2078375]
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- ☐ Z84573
S.aureus dihydropteroate synthase gene
gi|2058355|emb|Z84573.1|SADHPS01 [2058355]
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- ☐ AB001896
Staphylococcus aureus DNA for sigma70 operon, complete cds
gi|1943991|dbj|AB001896.1|AB001896 [1943991]
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- ☐ Y07645
S.aureus sigB gene
gi|1934986|emb|Y07645.1|SASIGFACB [1934986]
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- ☐ U92441
Staphylococcus aureus alkyl hydroperoxide reductase subunit C (aphC) and subunit F (aphF) genes, complete cds
gi|1916315|gb|U92441.1|SAU92441 [1916315]
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- ☐ U91741
Staphylococcus aureus teichoic acid biosynthesis TagB gene, partial cds and TagX and TagD genes, complete cds
gi|1913904|gb|U91741.1|SAU91741 [1913904]
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- ☐ U29454
Staphylococcus aureus penicillin binding protein 4 (pbpD) gene, complete cds
gi|1905928|gb|U29454.1|SAU29454 [1905928]
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☐ U29478

Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, complete cds
gi|1841513|gb|U29478.1|SAU29478 [1841513]

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Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds
gi|1657639|gb|U73374.1|SAU73374 [1657639]
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☐ L42945

Staphylococcus aureus lytS and lytR genes, complete cds
gi|1854576|gb|L42945.1|STALYTS [1854576]
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☐ U38429

Staphylococcus aureus chloramphenicol resistance plasmid pKH7, complete sequence
gi|1731451|gb|U38429.1|SAU38429 [1731451]
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☐ U81980

Staphylococcus aureus plasmid pKH4 replication protein Rep (rep) and quaternary ammonium compounds resistance protein Qac genes, complete cds
gi|1848267|gb|U81980.1|SAU81980 [1848267]
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☐ X55185

S. aureus hla gene for truncated alpha-toxin
gi|46745|emb|X55185.1|SATAT [46745]
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☐ V01278

S.aureus plasmid pE194 ORF's A,B,C,D,E, and F
gi|46555|emb|V01278.1|SAE194 [46555]
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- ☐ U31979
Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds
gi|987495|gb|U31979.1|SAU31979 [987495]
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- ☐ X91786
S.aureus abcA, pbp4, and tagD genes
gi|1262135|emb|X91786.1|SAPBP4GEN [1262135]
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- ☐ U36912
Staphylococcus aureus plasmid J3356::POX7;3, complete sequence
gi|1045528|gb|U36912.1|SAU36912 [1045528]
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- ☐ U36911
Staphylococcus aureus plasmid J3356::POX7;1, complete sequence
gi|1045526|gb|U36911.1|SAU36911 [1045526]
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- ☐ U36910
Staphylococcus aureus plasmid J3358, complete sequence
gi|1045523|gb|U36910.1|SAU36910 [1045523]
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- ☐ U64885
Staphylococcus aureus ribonuclease P RNA (rnpB) gene, partial sequence
gi|1498078|gb|U64885.1|SAU64885 [1498078]
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- ☐ U76872
Staphylococcus aureus isolate EMRSA-9 coagulase gene, VNTR sequence, sequence tagged site
gi|1753154|gb|U76872.1|SAU76872 [1753154]
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- ☐ U76871
Staphylococcus aureus isolate EMRSA-9 coagulase gene, VNTR sequence, sequence tagged site
gi|1753153|gb|U76871.1|SAU76871 [1753153]
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- ☐ U76870
Staphylococcus aureus isolate EMRSA-2 coagulase gene, VNTR sequence, sequence tagged site
gi|1753152|gb|U76870.1|SAU76870 [1753152]
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 - ☐ U76869
Staphylococcus aureus isolate EMRSA-2 coagulase gene, VNTR sequence, sequence tagged site
gi|1753151|gb|U76869.1|SAU76869 [1753151]
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 - ☐ U76868
Staphylococcus aureus isolate EMRSA-16 coagulase gene, VNTR sequence, sequence tagged site
gi|1753150|gb|U76868.1|SAU76868 [1753150]
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 - ☐ U76867
Staphylococcus aureus isolate EMRSA-16 coagulase gene, VNTR sequence, sequence tagged site
gi|1753149|gb|U76867.1|SAU76867 [1753149]
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 - ☐ U76866
Staphylococcus aureus isolate EMRSA-15 coagulase gene, VNTR sequence, sequence tagged site
gi|1753148|gb|U76866.1|SAU76866 [1753148]
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 - ☐ U76865
Staphylococcus aureus isolate EMRSA-5 coagulase gene, VNTR sequence, sequence tagged site
gi|1753147|gb|U76865.1|SAU76865 [1753147]
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 - ☐ U76864
Staphylococcus aureus isolate EMRSA-12 coagulase gene, VNTR sequence, sequence tagged site
gi|1753146|gb|U76864.1|SAU76864 [1753146]
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- ☐ U76863
Staphylococcus aureus isolate EMRSA-6 coagulase gene, VNTR sequence, sequence tagged site
gi|1753145|gb|U76863.1|SAU76863 [1753145]
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- ☐ U76862
Staphylococcus aureus isolate EMRSA-10 coagulase gene, VNTR sequence, sequence tagged site
gi|1753144|gb|U76862.1|SAU76862 [1753144]
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- ☐ U76861
Staphylococcus aureus isolate Jevons coagulase gene, VNTR sequence, sequence tagged site
gi|1753143|gb|U76861.1|SAU76861 [1753143]
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- ☐ U76860
Staphylococcus aureus isolate EMRSA-3 coagulase gene, VNTR sequence, sequence tagged site
gi|1753142|gb|U76860.1|SAU76860 [1753142]
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- ☐ U76859
Staphylococcus aureus isolate EMRSA-14 coagulase gene, VNTR sequence, sequence tagged site
gi|1753141|gb|U76859.1|SAU76859 [1753141]
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- ☐ U76858
Staphylococcus aureus German coagulase gene, VNTR sequence, sequence tagged site
gi|1753140|gb|U76858.1|SAU76858 [1753140]
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- ☐ U76857
Staphylococcus aureus isolate ps42e coagulase gene, VNTR sequence, sequence tagged site
gi|1753139|gb|U76857.1|SAU76857 [1753139]
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- ☐ U76856
Staphylococcus aureus isolate EMRSA-7 coagulase gene, VNTR sequence, sequence tagged site
gi|1753138|gb|U76856.1|SAU76856 [1753138]
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- ☐ U76855
Staphylococcus aureus isolate EMRSA-1 coagulase gene, VNTR sequence, sequence tagged site
gi|1753137|gb|U76855.1|SAU76855 [1753137]
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- ☐ U76854
Staphylococcus aureus isolate EMRSA-4 coagulase gene, VNTR sequence, sequence tagged site
gi|1753136|gb|U76854.1|SAU76854 [1753136]
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- ☐ U76853
Staphylococcus aureus isolate EMRSA-1 coagulase gene, VNTR sequence, sequence tagged site
gi|1753135|gb|U76853.1|SAU76853 [1753135]
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- ☐ U76852
Staphylococcus aureus isolate EMRSA-11 coagulase gene, VNTR sequence, sequence tagged site
gi|1753134|gb|U76852.1|SAU76852 [1753134]
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- ☐ U76851
Staphylococcus aureus isolate EMRSA-15 coagulase gene, VNTR sequence, sequence tagged site
gi|1753133|gb|U76851.1|SAU76851 [1753133]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), or [8 nucleotide neighbors](#))
- ☐ U76850
Staphylococcus aureus isolate ps 71 coagulase gene, VNTR sequence, sequence tagged site
gi|1753132|gb|U76850.1|SAU76850 [1753132]
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- ☐ U76849
Staphylococcus aureus isolate EMRSA-13 coagulase gene, VNTR sequence, sequence tagged site
gi|1753131|gb|U76849.1|SAU76849 [1753131]
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- ☐ U76848
Staphylococcus aureus isolate EMRSA-15 coagulase gene, VNTR sequence, sequence tagged

site

gi|1753130|gb|U76848.1|SAU76848 [1753130]

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☐ U76847

Staphylococcus aureus isolate EMRSA-15 coagulase gene, VNTR sequence, sequence tagged site

gi|1753129|gb|U76847.1|SAU76847 [1753129]

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Y09929

S.aureus rsbU, rsbV, rsbW & sigB genes

gi|1729791|emb|Y09929.1|SAUŠIGB [1729791]

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Y09570

S.aureus femD gene

gi|1684748|emb|Y09570.1|SAFEMD [1684748]

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☐ X95848

S.aureus fnbA gene

gi|1204145|emb|X95848.1|SAFNBA [1204145]

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☐ Y09428

S.aureus rpoC gene

gil1684750|emb|Y09428.1|SARPOCGE1 [1684750]

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☐ S76611

{*dru* element, hypervariable region, methicillin resistance determinant} [Staphylococcus aureus, MRSA, HVR genotype B, Genomic, 411 nt]

gi|913625|gb|S76611.1|S76611 [913625]

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☐ S76213

asp23=alkaline shock protein 23 {methicillin resistant} [Staphylococcus aureus, 912, Genomic, 1360 nt]

gi|894288|gb|S76213.1|S76213 [894288]

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☐ S75707

mec A {5' region, mutation IV} [Staphylococcus aureus, methicillin-resistant MR108, Genomic Mutant, 67 nt]
gi|913672|gb|S75707.1|S75707 [913672]
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☐ S75706

mec A {5' region, mutation III} [Staphylococcus aureus, methicillin-resistant MR108, Genomic Mutant, 67 nt]
gi|913671|gb|S75706.1|S75706 [913671]
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☐ S75705

mec A {5' region, mutation II} [Staphylococcus aureus, methicillin-resistant MR108, Genomic Mutant, 67 nt]
gi|913670|gb|S75705.1|S75705 [913670]
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☐ S76270

16S rRNA {16S-23S ribosomal RNA intergenic region} [Staphylococcus aureus, clinical isolate, Genomic, 94 nt]
gi|894286|gb|S76270.1|S76270 [894286]
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☐ S72497

plc=beta-hemolysin [Staphylococcus aureus, 126/89, Genomic, 1308 nt]
gi|619316|gb|S72497.1|S72497 [619316]
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☐ S72488

hemB=prophobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]
gi|632815|gb|S72488.1|S72488 [632815]
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citations 301-350 displayed (out of 558 found), page 7 of 12

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- ☐ S74031
norA=NorA {ISP794} [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]
gi|693734|gb|S74031.1|S74031 [693734]
(View [GenBank report](#), [FASTA report](#), [ASN.1 report](#), [Graphical view](#), [1 MEDLINE link](#), [1 protein link](#), or [3 nucleotide neighbors](#))
- ☐ S67449
tet(K)=tetracycline efflux protein [Staphylococcus aureus, pT181, Plasmid, 1380 nt]
gi|456769|gb|S67449.1|S67449 [456769]
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- ☐ U75367
Staphylococcus aureus transposon Tn551 transposase gene, partial cds
gi|1673526|gb|U75367.1|SATN551S2 [1673526]
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- ☐ U75368
Staphylococcus aureus transposon Tn551 transposase gene, partial cds
gi|1673524|gb|U75368.1|SATN551S1 [1673524]
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- ☐ U31175
Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds
gi|1644432|gb|U31175.1|SAU31175 [1644432]
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- ☐ X53096
S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease
gi|46616|emb|X53096.1|SAMTRE [46616]
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- ☐ X53951
S.aureus plasmid pSH6 DNA for insertion sequences IS257-2, IS257-3 and IS256

gi|46598|emb|X53951.1|SAIS2572 [46598]
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☐ X53952

S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 and IS256
gi|46596|emb|X53952.1|SAIS2571 [46596]
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☐ X03408

Staphylococcus aureus plasmid pUB110dB sequence
gi|46495|emb|X03408.1|SA110KAR [46495]
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☐ U50629

Staphylococcus aureus nicking enzyme (nes) gene, complete cds
gi|1245473|gb|U50629.1|SAU50629 [1245473]
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☐ U38656

Staphylococcus aureus tetracycline resistance plasmid pKH1, tet gene, complete cds
gi|1580803|gb|U38656.1|SAU38656 [1580803]
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☐ U58139

Staphylococcus aureus beta-lactamase (blaz) gene, complete cds
gi|1575124|gb|U58139.1|SAU58139 [1575124]
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☐ A31894

S.aureus pUB110 Ble gene
gi|1567207|emb|A31894.1|A31894 [1567207]
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☐ L42943

Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pckA) gene, complete cds
gi|860731|gb|L42943.1|STAPEPCK [860731]
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☐ U51474

Staphylococcus aureus truncated streptothricin acetyl transferase (sat) and 3'5'-aminoglycoside phosphotransferase (aphA-3) genes, complete cds
gi|1272325|gb|U51474.1|SAU51474 [1272325]

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☐ U50077

Staphylococcus aureus multidrug resistance plasmid pKH8 replication protein (rep) gene, qacC' gene, and multidrug resistance protein (qacC) gene, complete cds

gi|1236637|gb|U50077.1|SAU50077 [1236637]

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☐ U38428

Staphylococcus aureus tetracycline resistance plasmid pKH6, complete sequence

gi|1052997|gb|U38428.1|SAU38428 [1052997]

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☐ U66665

Staphylococcus aureus DNA fragment with class II promoter activity

gi|1519432|gb|U66665.1|SAU66665 [1519432]

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☐ U66664

Staphylococcus aureus DNA fragment with class II promoter activity

gi|1519431|gb|U66664.1|SAU66664 [1519431]

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☐ U66663

Staphylococcus aureus DNA fragment with class II promoter activity

gi|1519430|gb|U66663.1|SAU66663 [1519430]

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☐ X87104

S.aureus mdr, pbp4 and taqD genes (SG511-55 isolate)

gi|1125684|emb|X87104.1|SADNAS55 [1125684]

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☐ X87105

S.aureus mdr, pbp4 and taqD genes (PVI-25 isolate)

gi|1125680|emb|X87105.1|SADNAS25 [1125680]

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☐ X89233

S.aureus DNA for rpoC gene

gi|1495790|emb|X89233.1|SARPOCGEN [1495790]

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66663 49920460

- ☐ M28521
Staphylococcus aureus enterotoxin D (entD) gene, complete cds
gi|1492109|gb|M28521.1|STAENTD [1492109]
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- ☐ U54636
Staphylococcus aureus protein A, complete cds
gi|1480566|gb|U54636.1|SAU54636 [1480566]
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- ☐ U46541
Staphylococcus aureus sarA gene, complete cds
gi|1477531|gb|U46541.1|SAU46541 [1477531]
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- ☐ L14017
Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds
gi|1408062|gb|L14017.1|STAMECRA [1408062]
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- ☐ U60589
Staphylococcus aureus novel antigen gene, complete cds
gi|1407783|gb|U60589.1|SAU60589 [1407783]
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- ☐ Z48003
S.aureus gene for DNA polymerase III
gi|642269|emb|Z48003.1|SADNAPOL3 [642269]
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- ☐ M37889
Staphylococcus aureus replication (rep), control of replication (cop), and resistance protein (QacC) genes, complete cds
gi|153091|gb|M37889.1|STAREPQAC [153091]
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- ☐ V01281
S.aureus mRNA for nuclease
gi|46623|emb|V01281.1|SANUCX [46623]
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- ☐ X97985
S.aureus orfs 1,2,3 & 4
gi|1340127|emb|X97985.1|SA1234 [1340127]
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- ☐ X00127
Staphylococcus aureus S-phi-C gene for staphylokinase
gi|47425|emb|X00127.1|SPSAK1 [47425]
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- ☐ X03286
Staphylococcus aureus mutant strain V1 spa gene for protein A
gi|46774|emb|X03286.1|SAV1SPA [46774]
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- ☐ X62282
S.aureus target site DNA for IS431 insertion
gi|46769|emb|X62282.1|SATSIS431 [46769]
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- ☐ X01645
Staphylococcus aureus (Wood 46) gene for alpha-toxin
gi|46763|emb|X01645.1|SATOXA [46763]
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- ☐ X16471
Staphylococcus aureus transposon Tn4002 blaZ gene for beta-lactamase
gi|46761|emb|X16471.1|SATNBLAZ [46761]
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- ☐ X52734
S.aureus Tn552 transposable element
gi|46754|emb|X52734.1|SATN552 [46754]
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- ☐ X13290
Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003
gi|46747|emb|X13290.1|SATN4003 [46747]
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- ☐ X66088
S.aureus tRNA-Asp gene

gi|46744|emb|X66088.1|SATASP [46744]

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☐ Z30588

S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein

gi|459255|emb|Z30588.1|SASTPSMP [459255]

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☐ X16457

Staphylococcus aureus gene for staphylocoagulase

gi|46736|emb|X16457.1|SASTPHLC [46736]

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☐ X00342

Staphylococcus aureus 3' end of the gene for protein A

gi|46694|emb|X00342.1|SASPAY [46694]

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☐ V01287

Staphylococcus aureus gene (spa) fragment encoding protein A

gi|46692|emb|V01287.1|SASPAX [46692]

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☐ X61307

Staphylococcus aureus spa gene for protein A

gi|46690|emb|X61307.1|SASPAPA [46690]

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☐ Y00356

Staphylococcus aureus V8 serine protease gene

gi|46686|emb|Y00356.1|SASP [46686]

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☐ X06603

Staphylococcus aureus phage 42D for staphylokinase

gi|46676|emb|X06603.1|SASAK42D [46676]

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☐ X93205

S.aureus ptsH and ptsI genes

gi|1070384|emb|X93205.1|SAPTSHI [1070384]

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nucleotide neighbors)

☐ X64172

S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains

gi|677848|emb|X64172.1|SARPLRPO [677848]

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☐ X72700

S.aureus genes for S and F components of Panton-Valentine leucocidins

gi|551668|emb|X72700.1|SAPVLSF [551668]

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- ☐ X60827
S.aureus (plasmid pSCS6) cat gene for chloramphenicol acetyltransferase
gi|46651|emb|X60827.1|SAPSCS6 [46651]
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- ☐ X64389
S.aureus leuF-P83 gene for F component of leucocidin R
gi|488528|emb|X64389.1|SALEUF [488528]
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- ☐ X62288
S.aureus DNA for penicillin-binding protein 2
gi|483533|emb|X62288.1|SAPENBP2 [483533]
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- ☐ X55798
S.aureus plasmid pOX2000
gi|295833|emb|X55798.1|SAPOX2000 [295833]
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- ☐ X58434
S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase
gi|48871|emb|X58434.1|SAPDHDNA [48871]
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- ☐ X06627
Staphylococcus aureus plasmid pS194 sequence
gi|46643|emb|X06627.1|SAPS194 [46643]
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- ☐ X12831
Staphylococcus aureus chloramphenicol resistance plasmid pC223 DNA (nt 1250 - 3072)

gi|46637|emb|X12831.1|SAPC223A [46637]
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☐ X07371

Staphylococcus aureus plasmid pC223 basic replicon DNA
gi|46635|emb|X07371.1|SAPC223 [46635]
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☐ X02529

Staphylococcus aureus plasmid pC221 complete DNA sequence
gi|46630|emb|X02529.1|SAPC221 [46630]
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☐ Y00688

Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein
gi|46628|emb|Y00688.1|SAPBP [46628]
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☐ X04121

S. aureus PC1 beta-lactamase gene blaZ from plasmid pI258
gi|46626|emb|X04121.1|SAPBLAZ [46626]
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☐ X59477

S.aureus plasmid DNA for part of mupirocin resistance gene (XhoI site)
gi|46621|emb|X59477.1|SAMUPIRES [46621]
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☐ X59478

S.aureus plasmid DNA for mupirocin resistance gene (NcoI-NcoI fragment)
gi|46619|emb|X59478.1|SAMUPIREI [46619]
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☐ X63598

S.aureus mecR1 and mecI genes
gi|46612|emb|X63598.1|SAMECR1I [46612]
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☐ X52593

S. aureus mecA gene for PBP2' (penicillin binding protein 2')
gi|46610|emb|X52593.1|SAMECAPB [46610]
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6636949469

- ☐ X76490
S.aureus (bb270) glnA and glnR genes
gi|1134885|emb|X76490.1|SAGLNAR [1134885]
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- ☐ X81586
S.aureus hlgA, hlgB and hlgC genes
gi|550421|emb|X81586.1|SAHLGABC [550421]
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- ☐ X72014
S.aureus fib gene for fibrinogen-binding protein
gi|311975|emb|X72014.1|SAFIBB [311975]
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- ☐ X72013
S.aureus fib gene for fibrinogen-binding protein
gi|311973|emb|X72013.1|SAFIBA [311973]
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- ☐ X71437
S.aureus genes gyrB, gyrA and recF (partial)
gi|296393|emb|X71437.1|SAGYRREC [296393]
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- ☐ X62992
S.aureus fnbB gene for fibronectin binding protein B
gi|49040|emb|X62992.1|SAFNBB [49040]
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- ☐ X52594
S. aureus hypervariable region, 3' to mecA gene
gi|48712|emb|X52594.1|SAHVR [48712]
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- ☐ X14827
Staphylococcus aureus lacC and lacD genes
gi|46604|emb|X14827.1|SALACCD [46604]
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- ☐ X13404

Staphylococcus aureus hlb gene for beta-hemolysin

gi|46586|emb|X13404.1|SAHLB [46586]

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☐ X17301

S.aureus DNA for hld gene and for part of agr gene

gi|46585|emb|X17301.1|SAHDLAGR [46585]

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☐ X17688

S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end

gi|46579|emb|X17688.1|SAFEMA [46579]

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☐ X03097

Staphylococcus aureus plasmid pE194 mRNA for ermC leader region

gi|46574|emb|X03097.1|SAERMCTR [46574]

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☐ Z16422

S.aureus dfrB gene for dihydrofolate reductase

gi|671631|emb|Z16422.1|SADIRED [671631]

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☐ Z33409

S.aureus (C6-coa-EM) coagulase gene repeat region

gi|495298|emb|Z33409.1|SACOAGR6 [495298]

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☐ Z33408

S.aureus (C50-coa-E) coagulase gene repeat region

gi|495297|emb|Z33408.1|SACOAGR5 [495297]

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☐ Z33407

S.aureus (C35-coa-E) coagulase gene repeat region

gi|495296|emb|Z33407.1|SACOAGR4 [495296]

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☐ Z33406

S.aureus (C26-coa-E) coagulase gene repeat region

gi|495295|emb|Z33406.1|SACOAGR3 [495295]

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☐ Z33405

S.aureus (C20-coa-E) coagulase gene repeat region

gi|495294|emb|Z33405.1|SACOAGR2 [495294]

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☐ Z33404

S.aureus (C14-coa-E) coagulase gene repeat region

gi|495293|emb|Z33404.1|SACOAGR1 [495293]

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☐ X75439

S.aureus plasmid encoded DNA, mup R gene

gi|438226|emb|X75439.1|SADNAMUPR [438226]

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☐ X62587

S.aureus ebr gene for ethidium bromide resistance protein

gi|49016|emb|X62587.1|SAEBRN20 [49016]

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☐ X54338

S.aureus plasmid pA22 ermC gene (5' region)

gi|46572|emb|X54338.1|SAERMC [46572]

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☐ X51661

S.aureus enterotoxin C3 gene (entC3)

gi|46570|emb|X51661.1|SAENTC3A [46570]

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☐ X05815

Staphylococcus enterotoxin C1 gene (entC1)

gi|46566|emb|X05815.1|SAENTC1 [46566]

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☐ X15574

Staphylococcus aureus plasmid gene for ethidium bromide resistance (ebr)

gi|46560|emb|X15574.1|SAEBR [46560]

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- ☐ Y07536
S. aureus genes for thymidylate synthetase and dihydrofolate reductase type S1 in plamid pABU
1
gi|46551|emb|Y07536.1|SADHFR [46551]
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- ☐ X02166
Staphylococcus plasmid pC221
gi|46545|emb|X02166.1|SACP221 [46545]
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- ☐ Z49245
S.aureus partial sod gene for superoxide dismutase
gi|806584|emb|Z49245.1|SA4220SOD [806584]
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- ☐ X16298
Staphylococcus aureus plasmid pI9789 DNA with binR and bin3 genes, derived from
transposon TN552
gi|398181|emb|X16298.1|SABINR3 [398181]
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- ☐ Z18852
S.aureus gene for clumping factor
gi|397525|emb|Z18852.1|SACFG [397525]
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- ☐ X68417
S.aureus gene for 16S rRNA
gi|312111|emb|X68417.1|SA16SRRN [312111]
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- ☐ X68425
S.aureus gene for 23S rRNA
gi|288516|emb|X68425.1|SA23SRRN [288516]
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- ☐ X17679
Staphylococcus aureus coa gene for coagulase
gi|46539|emb|X17679.1|SACOA [46539]
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☐ X63072

S.aureus DNA for cat transcription terminator region

gi|46538|emb|X63072.1|SACÀTTERM [46538]

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☐ X02872

Staphylococcus aureus plasmid pUB112 CAT-gene for chloramphenicol acetyltransferase

gi|46536|emb|X02872.1|SACATG [46536]

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- ☐ V01277
Staphylococcus aureus plasmid pC194. Includes gene for chloramphenicol acetyl transferase and three further genes (one of which is necessary for replication)
gi|46531|emb|V01277.1|SAC194 [46531]
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- ☐ X52543
S.aureus agrA, agrB and hld genes
gi|46505|emb|X52543.1|SAAGRAB [46505]
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- ☐ A19943
SEQ ID NO: 8, strain 1335 nucleotide probe
gi|580681|emb|A19943.1|A19943 [580681]
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- ☐ A19942
SEQ ID NO: 7, strain 06231 nucleotide probe
gi|580680|emb|A19942.1|A19942 [580680]
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- ☐ A19941
SEQ ID NO: 6, strain 215C nucleotide probe
gi|580679|emb|A19941.1|A19941 [580679]
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- ☐ A19940
SEQ ID NO: 5, strain 214 nucleotide probe
gi|580678|emb|A19940.1|A19940 [580678]
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- ☐ A19939

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SEQ ID NO: 3, strain A216 nucleotide probe

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SEQ ID NO: 2, strain 00646 nucleotide probe

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SEQ ID NO: 1, strain 05723 nucleotide probe

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sau3AI R and sau3AI M coding region

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S.aureus DNA (pSDF203) for fibronectin binding protein (partial)

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nucleotide neighbors)

S.aureus DNA (pSDF102) for fibronectin binding protein (partial)

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S.aureus DNA for fibronectin binding protein (partial)

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S.aureus DNA for fibronectin binding protein (partial)

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nucleotide neighbors)

- ☐ A12904
S.aureus DNA for fibronectin binding protein (partial)
gi|512501|emb|A12904.1|A12904 [512501]
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- ☐ A12903
S.aureus DNA for fibronectin binding protein (partial)
gi|512499|emb|A12903.1|A12903 [512499]
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- ☐ A12902
S.aureus DNA for fibronectin binding protein (partial)
gi|512497|emb|A12902.1|A12902 [512497]
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- ☐ A12901
S.aureus DNA for fibronectin binding protein (partial)
gi|512495|emb|A12901.1|A12901 [512495]
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- ☐ A12900
S.aureus DNA for fibronectin binding protein (partial)
gi|512494|emb|A12900.1|A12900 [512494]
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- ☐ A12899
S.aureus DNA for fibronectin binding protein (partial)
gi|512492|emb|A12899.1|A12899 [512492]
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- ☐ A12898
S.aureus DNA for fibronectin binding protein (partial)
gi|512490|emb|A12898.1|A12898 [512490]
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- ☐ A12897
S.aureus DNA for fibronectin binding protein (partial)
gi|512488|emb|A12897.1|A12897 [512488]
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- ☐ A12896

S.aureus DNA for fibronectin binding protein (partial)

gi|512486|emb|A12896.1|A12896 [512486]

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☐ A09523

S.aureus Arp 4 gene

gi|412258|emb|A09523.1|A09523 [412258]

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☐ A04518

S.aureus gene for structural protein A, duplicate

gi|412213|emb|A04518.1|A04518 [412213]

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☐ A04517

S.aureus gene for structural protein A

gi|412212|emb|A04517.1|A04517 [412212]

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☐ A04512

S.aureus gene for structural protein A

gi|412210|emb|A04512.1|A04512 [412210]

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☐ L41499

Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds

gi|765069|gb|L41499.1|STAATL [765069]

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☐ U19770

Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds

gi|790572|gb|U19770.1|SAU19770 [790572]

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☐ X53818

S. aureus IS431mec gene associated with methicillin resistance

gi|46601|emb|X53818.1|SAIS431M [46601]

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☐ M20129

Staphylococcus aureus vgh gene, complete cds

gi|153076|gb|M20129.1|STAPVGHG [153076]

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- ☐ L43098
Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA
gi|1280355|gb|L43098.1|INSTN5405R [1280355]
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- ☐ L43082
Transposon Tn5405 and insertion sequence IS1182 (from Staphylococcus aureus) ORFA and transposase gene, complete cds
gi|1280353|gb|L43082.1|INSTN5405L [1280353]
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- ☐ X03216
Staphylococcus aureus transposon Tn554
gi|43726|emb|X03216.1|ISTN554 [43726]
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- ☐ X70648
S.aureus 16S rRNA (partial)
gi|46498|emb|X70648.1|SA16S [46498]
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- ☐ U51133
Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds
gi|1255261|gb|U51133.1|SAU51133 [1255261]
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- ☐ U51132
Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-succinylbenzoic acid synthetase (menc) genes, complete cds
gi|1255258|gb|U51132.1|SAU51132 [1255258]
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- ☐ X02588
S. aureus Tn554 spc gene for sp adenylyltransferase AAD(9) (sp = spectinomycin)
gi|46696|emb|X02588.1|SASPCG [46696]
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- ☐ X61716
S.aureus hlb gene encoding sphingomyelinase
gi|46590|emb|X61716.1|SAHLBG [46590]
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- ☐ X61719
S.aureus phi-13 lysogen right chromosome/bacteriophage DNA junction
gi|46625|emb|X61719.1|SAP13RJNC [46625]
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- ☐ X61718
S.aureus phi-13 lysogen left chromosomal/bacteriophage DNA junction
gi|46624|emb|X61718.1|SAP13LJNC [46624]
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- ☐ X67743
S.aureus (strain 42CR3-L) right junction DNA
gi|46518|emb|X67743.1|SAATTSB2 [46518]
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- ☐ X67742
S.aureus (strain 42CR3-L) left junction DNA
gi|46517|emb|X67742.1|SAATTSB1 [46517]
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- ☐ X67741
S.aureus (strain A3CR3-L) left junction DNA
gi|46516|emb|X67741.1|SAATTSA2 [46516]
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- ☐ X67740
S.aureus (strain A3CR3-L) right junction DNA
gi|46515|emb|X67740.1|SAATTSA1 [46515]
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- ☐ X67738
S.aureus (strain 80CR3) attB gene
gi|46514|emb|X67738.1|SAATTBA [46514]
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- ☐ U02910
Staphylococcus aureus ATCC 25923 16S rRNA gene, partial sequence
gi|455053|gb|U02910.1|SAU02910 [455053]
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- ☐ AH003349
Transposon IS431 (from S.aureus penicillinase plasmid pI524), 5' copy
gi|154887|gb|AH003349.1|SEG_TRN431 [154887]
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 M11118

S.aureus enterotoxin B gene, complete cds
gi|152999|gb|M11118.1|STAENTB [152999]

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- ☐ M18086
S.aureus transposon 4001 aacA-aphD aminoglycoside resistance gene, complete cds, and right and left IS256 transposase genes
gi|152946|gb|M18086.1|STAAGLSRA [152946]
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- ☐ U19459
Staphylococcus aureus acetyltransferase VAT B (vat B) gene, complete cds
gi|1181626|gb|U19459.1|SAU19459 [1181626]
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- ☐ U35773
Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds
gi|1016769|gb|U35773.1|SAU35773 [1016769]
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- ☐ U26702
Staphylococcus aureus recombination site for plasmid pS1
gi|849134|gb|U26702.1|SAU26702 [849134]
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- ☐ U21221
Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds
gi|705405|gb|U21221.1|SAU21221 [705405]
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- ☐ U36379
Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds
gi|1020316|gb|U36379.1|SAU36379 [1020316]
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- ☐ U06451
Staphylococcus aureus proline permease homolog (putP) gene, complete cds
gi|458419|gb|U06451.1|SAU06451 [458419]
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☐ U35036

Staphylococcus aureus R-plasmid pSBK203 replication initiation protein gene, chloramphenicol acetyltransferase gene, and Pre protein gene, complete cds
gi|1015405|gb|U35036.1|SAU35036 [1015405]
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☐ U20794

Staphylococcus aureus fibrinogen binding protein (fbpA) gene, complete cds
gi|915307|gb|U20794.1|SAU20794 [915307]
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☐ L25426

Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds
gi|409240|gb|L25426.1|STAPBP2X [409240]
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☐ M86227

Staphylococcus aureus DNA gyrase B subunit (gyrB) RecF homologue (recF) and DNA gyrase A subunit (gyrA) gene, complete cds
gi|153083|gb|M86227.1|STARECF [153083]
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☐ M63176

Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds
gi|153060|gb|M63176.1|STAPCRA [153060]
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☐ L11998

Staphylococcus aureus conjugative transfer gene complex (trs)
gi|310606|gb|L11998.1|STATRSC [310606]
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☐ L05004

Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds
gi|152954|gb|L05004.1|STAAROA [152954]
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☐ L42764

Staphylococcus aureus (clone pS120+) DNA fragment
gi|852065|gb|L42764.1|STAFRA [852065]
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652065 "032695" 409240

neighbors)

- ☐ M32103
Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds
gi|845685|gb|M32103.1|STALACR [845685]
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- ☐ U10927
Staphylococcus aureus M type 1 capsular polysaccharide biosynthesis (capA, capB, capC, capD, capE, capF, capG, capH, capI, capJ, capK, capL, capM) genes, complete cds
gi|567035|gb|U10927.1|SAU10927 [567035]
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- ☐ AH003057
Staphylococcus aureus dihydrolipoamide dehydrogenase E2 subunit gene, partial cds
gi|152993|gb|AH003057.1|SEG_STADLDE [152993]
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- ☐ M73535
Staphylococcus aureus dihydrolipoamide dehydrogenase E2 subunit gene, 3' end and dihydrolipoamide dehydrogenase E3 subunit gene, 5' end
gi|152992|gb|M73535.1|STADLDE2 [152992]
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- ☐ M73536
Staphylococcus aureus dihydrolipoamide dehydrogenase E2 subunit gene, partial cds
gi|152991|gb|M73536.1|STADLDE1 [152991]
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- ☐ U20782
Staphylococcus aureus staphylococcal accessory regulator A (sarA) gene, complete cds
gi|684949|gb|U20782.1|SAU20782 [684949]
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- ☐ L37598
Staphylococcus auricularis 16S ribosomal RNA (16S rRNA) gene
gi|576604|gb|L37598.1|STARGDC [576604]
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- ☐ L37597
Staphylococcus aureus 16S ribosomal RNA (16S rRNA) gene
gi|576603|gb|L37597.1|STARGDB [576603]
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684949 576604 576603

neighbors)

- ☐ L36472
Staphylococcus aureus lysyl-tRNA synthetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S rRNA) gene, 23S ribosomal RNA (23S rRNA) gene
gi|567883|gb|L36472.1|STA5SRR [567883]
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- ☐ L25288
Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds
gi|561878|gb|L25288.1|STAGYRASL [561878]
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- ☐ L25893
Staphylococcus aureus recA gene, complete cds
gi|463284|gb|L25893.1|STARECAA [463284]
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- ☐ K02687
S.aureus 5S ribosomal RNA
gi|176018|gb|K02687.1|STARRASA [176018]
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- ☐ L23109
Staphylococcus aureus recombinase (sin) gene, complete cds
gi|495088|gb|L23109.1|STASINA [495088]
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- ☐ L07778
Staphylococcus aureus acetyltransferase (vat) gene, complete cds
gi|398084|gb|L07778.1|STAVAT [398084]
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- ☐ M90056
Staphylococcus aureus plasmid ATP-binding protein (vga) gene, complete cds
gi|153124|gb|M90056.1|STAVGA [153124]
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- ☐ J02615
S.aureus toxic shock syndrome toxin-1 gene, complete cds
gi|153122|gb|J02615.1|STATSST1 [153122]
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protein link, or 4 nucleotide neighbors)

☐ M18970

S.aureus enterotoxin A (entA) gene, complete cds

gi|153120|gb|M18970.1|STATOXAA [153120]

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☐ K02985

S.aureus (strain RN450) transposon Tn554 insertion site

gi|153118|gb|K02985.1|STATNIS5 [153118]

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☐ M21136

S.aureus tetracycline resistance (tetM) gene, complete cds

gi|153114|gb|M21136.1|STATETM [153114]

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☐ M10501

S.aureus/transposon Tn551 left junction C

gi|153113|gb|M10501.1|STAT551C [153113]

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☐ AH000935

S.aureus/transposon Tn551 left junction B

gi|153112|gb|AH000935.1|SEG_STAT551B [153112]

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☐ M10500

S.aureus/transposon Tn551 right junction B

gi|153111|gb|M10500.1|STAT551B2 [153111]

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☐ M10499

S.aureus/transposon Tn551 left junction B

gi|153110|gb|M10499.1|STAT551B1 [153110]

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☐ AH000934

S.aureus/transposon Tn551 left junction A

gi|153109|gb|AH000934.1|SEG_STAT551A [153109]

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☐ M10498

S.aureus/transposon Tn551 right junction A

gi|153108|gb|M10498.1|STAT551A2 [153108]

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- ☐ M10497
S.aureus/transposon Tn551 left junction A
gi|153107|gb|M10497.1|STAT551A1 [153107]
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- ☐ M18264
S.aureus staphylococcal protein A (SPA) gene, complete cds
gi|153105|gb|M18264.1|STASPAA [153105]
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- ☐ J01786
S.aureus spa gene coding for protein A, complete cds
gi|153103|gb|J01786.1|STASPA [153103]
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- ☐ M33833
S.aureus enterotoxin B (seb) gene, 5' flank
gi|153101|gb|M33833.1|STASEB [153101]
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- ☐ M32470
S.aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes, complete cds
gi|153098|gb|M32470.1|STASAU3AIM [153098]
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- ☐ M20270
S.aureus neomycin resistance gene, partial cds, and bleomycin resistance gene, complete cds
gi|153095|gb|M20270.1|STARESA [153095]
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- ☐ J03323
S.aureus plasmid pCW7 REP N protein (rep N) gene, complete cds
gi|153089|gb|J03323.1|STAREPNA [153089]
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- ☐ M33479
S.aureus ethidium resistance (ebr) and replication protein (repA) genes, complete cds
gi|153087|gb|M33479.1|STAREPEBR [153087]
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- ☐ M94061

Staphylococcus aureus recombination enzyme (recA) gene, partial cds

gi|153081|gb|M94061.1|STARECA [153081]

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☐ M37888

Staphylococcus aureus resistance protein (qacD) gene, complete cds

gi|153078|gb|M37888.1|STAQACD [153078]

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- ☐ M76714
Staphylococcus aureus peptidoglycan hydrolase gene, complete cds
gi|153066|gb|M76714.1|STAPEPHYD [153066]
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- ☐ M17123
S.aureus nuclease gene, partial cds
gi|153056|gb|M17123.1|STANUC [153056]
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- ☐ M97169
Staphylococcus aureus fluoroquinolone resistance protein (norA) gene, complete cds
gi|153054|gb|M97169.1|STANORAX [153054]
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- ☐ M81346
Staphylococcus aureus (methicillin resistant) leucocidin S-component (lukS) gene, complete cds
gi|475838|gb|M81346.1|STALUKS [475838]
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- ☐ M90693
Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds
gi|393265|gb|M90693.1|STAGEHLIP [393265]
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- ☐ M25257
Staphylococcus aureus (clone pUB10) beta-lactamase gene, complete cds
gi|341312|gb|M25257.1|STALACBAF [341312]
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- ☐ M25256
Staphylococcus aureus (clone pII3804) beta-lactamase gene, 5' end

gi|341311|gb|M25256.1|STALACBAE [341311]
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☐ M25255

Staphylococcus aureus (clone pI3796) beta-lactamase gene, 5' end
gi|341310|gb|M25255.1|STALACBAD [341310]
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☐ M25254

Staphylococcus aureus (clone pI1071) beta-lactamase gene, complete cds
gi|341309|gb|M25254.1|STALACBAC [341309]
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☐ M25253

Staphylococcus aureus (clone pS1) beta-lactamase gene, complete cds
gi|341308|gb|M25253.1|STALACBAB [341308]
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☐ M25252

Staphylococcus aureus (clone pPC1) beta-lactamase gene, complete cds
gi|341307|gb|M25252.1|STALACBAA [341307]
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☐ L01055

Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hlgC) genes, complete cds
gi|295153|gb|L01055.1|STAHLGA [295153]
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☐ M83994

Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds
gi|153044|gb|M83994.1|STALSP [153044]
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☐ J03947

S.aureus lincosaminide nucleotidyltransferase (linA) gene, complete cds
gi|153040|gb|J03947.1|STALINA [153040]
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☐ J03479

S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds
gi|153036|gb|J03479.1|STALACS [153036]

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☐ M64724

S.aureus tagatose 6-phosphate isomerase gene, complete cds

gi|153032|gb|M64724.1|STALACAA [153032]

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☐ M14372

S.aureus phage L54 attP site

gi|153031|gb|M14372.1|STAL54POP [153031]

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☐ M14371

S.aureus phage L54

gi|153030|gb|M14371.1|STAL54POB [153030]

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☐ M14374

S.aureus phage L54 attL site

gi|153029|gb|M14374.1|STAL54BOP [153029]

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☐ M15215

S.aureus phage L54 attB site

gi|153028|gb|M15215.1|STAL54BOB [153028]

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☐ M36694

B.amyloliquefaciens neutral protease gene, complete cds

gi|153026|gb|M36694.1|STAINVSA [153026]

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☐ M37915

S.aureus gyrase (gyrB and gryA) genes, 3' and 5' ends, respectively

gi|153023|gb|M37915.1|STAGYRAB [153023]

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☐ M12715

S.aureus geh gene encoding lipase (glycerol ester hydrolase)

gi|153019|gb|M12715.1|STAGEH [153019]

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- ☐ J04151
S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds
gi|153017|gb|J04151.1|STAFNBP [153017]
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- ☐ L22566
Staphylococcus aureus enterotoxin A gene
gi|349129|gb|L22566.1|STAENTAB [349129]
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- ☐ L13379
Staphylococcus aureus enterotoxin gene, 3' end
gi|295150|gb|L13379.1|STAENTEROF [295150]
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- ☐ L13378
Staphylococcus aureus enterotoxin gene, 3' end
gi|295148|gb|L13378.1|STAENTEROE [295148]
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- ☐ L13377
Staphylococcus aureus enterotoxin gene, 3' end
gi|295146|gb|L13377.1|STAENTEROD [295146]
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- ☐ L13376
Staphylococcus aureus enterotoxin gene, 3' end
gi|295144|gb|L13376.1|STAENTEROC [295144]
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- ☐ L13375
Staphylococcus aureus enterotoxin gene, 3' end
gi|295142|gb|L13375.1|STAENTEROB [295142]
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- ☐ L13374
Staphylococcus aureus enterotoxin gene, 3' end
gi|295140|gb|L13374.1|STAENTEROA [295140]
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- ☐ M17348

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S.aureus exfoliative toxin B (ETB), complete cds

gi|153011|gb|M17348.1|STAETB [153011]

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☐ M17357

S.aureus eta gene encoding epidermolytic toxin A, complete cds

gi|153007|gb|M17357.1|STAETAA [153007]

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☐ M17347

S.aureus exfoliative toxin A (ETA), complete cds

gi|153005|gb|M17347.1|STAETA [153005]

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☐ M28364

Staphylococcus aureus enterotoxin C3 gene, complete cds

gi|153003|gb|M28364.1|STAENTTXC [153003]

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☐ M21319

S.aureus enterotoxin type E (entE) gene, complete cds

gi|153001|gb|M21319.1|STAENTE [153001]

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☐ M63917

S.aureus epidermal cell differentiation inhibitor (EDIN) gene, complete cds

gi|152997|gb|M63917.1|STAEDIN [152997]

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☐ M58515

Staphylococcus aureus precursor protein and chloramphenicol acetyltransferase (CAT) genes, complete cds

gi|152980|gb|M58515.1|STACATA [152980]

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☐ L10909

Staphylococcus aureus tnpA gene, tnpB gene, tnpC gene, DS RF gene, complete cds's; cadmium resistance (cadA) gene, complete cds; E1-E2 cadmium efflux adenosine triphosphatase (cadC) gene, complete cds

gi|152973|gb|L10909.1|STACADRES [152973]

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☐ M15067

S.aureus beta-lactamase (blaZ) gene, 5' end

gi|152971|gb|M15067.1|STABLAZA [152971]

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☐ M92376

Staphylococcus aureus beta-lactamase repressor (BlaI) gene, complete cds

gi|152969|gb|M92376.1|STABLAIA [152969]

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☐ M62650

Staphylococcus aureus blaZ gene, 5' end; blaR1 gene, complete cds; blaI gene, complete cds; and binR gene, 5' end

gi|152964|gb|M62650.1|STABLA [152964]

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☐ M32312

S.aureus right arm of secondary Tn554 attachment site

gi|152959|gb|M32312.1|STAATTX [152959]

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☐ M20393

S.aureus bacteriophage phi-11 attachment site (attB)

gi|152958|gb|M20393.1|STAATTB [152958]

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☐ M90536

Staphylococcus aureus alpha-hemolysin gene, 3' end

gi|152952|gb|M90536.1|STAALPHYM [152952]

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☐ M21854

S.aureus agr gene encoding an accessory gene regulator protein, complete cds

gi|152950|gb|M21854.1|STAAGR [152950]

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☐ M36771

S.aureus aminocyclitol-3'-phosphotransferase gene, complete cds

gi|152944|gb|M36771.1|STAAAC [152944]

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☐ L14020

Staphylococcus aureus methicillin-resistance (mecR and mecI) genes, complete cds

gi|295157|gb|L14020.1|STAMECR [295157]

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655660403040

☐ M81736

Staphylococcus aureus collagen adhesin (cna) gene, complete cds

gi|387879|gb|M81736.1|STACNA [387879]

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☐ U11702

Staphylococcus aureus D4508 enterotoxin H (seh) gene, complete cds

gi|510691|gb|U11702.1|SAU11702 [510691]

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- ☐ L19300
Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank
gi|310601|gb|L19300.1|STAORFPHI [310601]
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 - ☐ L25372
Staphylococcus aureus exfoliative toxin A (eta) gene, complete cds
gi|409062|gb|L25372.1|STASETA [409062]
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 - ☐ L22565
Staphylococcus aureus FRI100 enterotoxin A (sea) gene
gi|349128|gb|L22565.1|STAENTAA [349128]
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 - ☐ M58516
Staphylococcus aureus precursor protein and chloramphenicol acetyltransferase (CAT) genes, complete cds
gi|152983|gb|M58516.1|STACATB [152983]
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 - ☐ U06462
Staphylococcus aureus SA4 FtsZ (ftsZ) gene, complete cds
gi|458427|gb|U06462.1|SAU06462 [458427]
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 - ☐ L19298
Staphylococcus aureus phosphatidylinositol-specific phospholipase C (plc) gene, complete cds
gi|425477|gb|L19298.1|STAPIPLC [425477]
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 - ☐ M80252

Staphylococcus aureus norA1199 gene (which mediates active efflux of fluoroquinolones), complete cds
gi|295163|gb|M80252.1|STANORA11 [295163]
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☐ L11530

Staphylococcus aureus transfer RNA sequence with two rRNAs
gi|310605|gb|L11530.1|STATRNAA [310605]
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1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	